

Fri Sep 28 10:45:04 2001

us-09-492-029-3.rag

Page 1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 28, 2001, 10:28:10 : Search time 34.79 Seconds
(without alignments)
592.474 Million cell updates/sec

Title: US-09-492-029-3
Perfect score: 1809
Sequence: 1 MGEWQLKOEAFQKQAD.....TADGMAVATGMSDFLKTWN 340

Scoring table:
Gapop 10.0, Gapext 0.5

Searched: 412676 seqs, 60623988 residues 412676

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A-Geneseq-0601: *
2: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT: *
3: /SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT: *
4: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT: *
5: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT: *
6: /SIDSB/gcgdata/geneseq/geneseq/AA1985.DAT: *
7: /SIDSB/gcgdata/geneseq/geneseq/AA1986.DAT: *
8: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT: *
9: /SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT: *
10: /SIDSB/gcgdata/geneseq/geneseq/AA1989.DAT: *
11: /SIDSB/gcgdata/geneseq/geneseq/AA1990.DAT: *
12: /SIDSB/gcgdata/geneseq/geneseq/AA1991.DAT: *
13: /SIDSB/gcgdata/geneseq/geneseq/AA1992.DAT: *
14: /SIDSB/gcgdata/geneseq/geneseq/AA1993.DAT: *
15: /SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT: *
16: /SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT: *
17: /SIDSB/gcgdata/geneseq/geneseq/AA1996.DAT: *
18: /SIDSB/gcgdata/geneseq/geneseq/AA1997.DAT: *
19: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT: *
20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT: *
21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT: *
22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT: *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1809	100.0	340	21	AA15168
2	1806	99.8	340	21	AA15170
3	1806	99.8	340	21	AA15171
4	1805	99.8	340	21	AA15172
5	1762	97.4	340	19	AA15169
6	1762	97.4	340	21	AA15173
7	1762	97.4	340	21	AA15174
8	1759	97.2	340	21	AA15175
9	1759	97.2	340	21	AA15176
10	1753	87.0	340	16	AA15177

12	1573	87.0	340	21	AA15168
13	1523	84.2	340	16	AA15169
14	1523	84.2	340	21	AA15170
15	1520.5	84.1	299	19	AA15171
16	1518.5	83.9	297	21	AA15172
17	1493	82.5	340	21	AA15173
18	1467	81.1	341	16	AA15174
19	1452	80.3	340	16	AA15175
20	1419	78.4	326	16	AA15176
21	946.5	52.3	353	21	AA15177
22	945.5	49.7	371	21	AA15178
23	901.5	45.8	295	22	AA15179
24	863.5	47.6	295	22	AA15180
25	860.5	45.2	277	21	AA15181
26	817	45.2	229	21	AA15182
27	655.5	36.2	267	21	AA15183
28	652.5	36.1	267	21	AA15184
29	639	35.3	423	16	AA15185
30	639	35.3	423	20	AA15186
31	639	35.3	423	21	AA15187
32	638	35.3	422	20	AA15188
33	635	35.1	422	20	AA15189
34	635	35.1	422	21	AA15190
35	609.5	33.7	223	22	AA15191
36	593	32.8	243	21	AA15192
37	571	31.6	166	21	AA15193
38	528	29.2	227	21	AA15194
39	528	29.2	227	21	AA15195
40	528	29.2	227	21	AA15196
41	421.5	23.3	403	21	AA15197
42	421.5	23.3	403	21	AA15198
43	308	17.0	471	21	AA15199
44	299	16.5	471	21	AA15200
45	299	16.5	471	21	AA15201

ALIGNMENTS

RESULT 1	AA15168	standard; Protein; 340 AA.
ID	AA15168	
AC	AA15168	
XX	12-DEC-2000	(first entry)
DE	Rat Taste Cell	specific G-protein beta 3 subunit.
DE	Rat: Taste Cell	specific G-protein beta 3 subunit; TC-Gbeta3;
KW	taste transduction pathway; pharmaceutical; food industry.	
XX	Rattus sp.	
OS	WO200045179-A2.	
PN	03-AUG-2000.	
PD	26-JAN-2000; 2000WO-US02218.	
PF	27-JAN-1999; 99US-0117404.	
PR	(REGC) UNIV CALIFORNIA.	
XX	Zuker CS, Adler JE, Lindemeyer J;	
PI	WPI: 2000-499361/44.	
DR	N-PSDB: AAA74590.	
XX	Identifying a compound that modulates sensory signaling in sensory	
XX	cells for use in pharmaceutical and food industries comprises	
PT	contacting the compound with a sensory cell specific G-protein beta	
PT	polypeptide	

Human Hgb1 G-prot
WD-40 domain-contg
Human Hgb2 G-prot
Human G-protein be
Human G-protein be
Mouse Mgb4 G-prot
WD-40 domain-contg
WD-40 domain-contg
WD-40 domain-contg
Human cell cycle r
Mouse Mgb5 G-prot
Human pancreatic c
Gene 45 human secr
Human secreted pro
Arabidopsis thalia
Gene 45 human secr
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Yeast G protein be
WD-40 domain-contg
Steap/beta intera
Yeast G protein be
Yeast G protein be
Yeast Ste4 protein
Human secreted pro
Breast and ovarian
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Human GTP-binding
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia

PS Claim 1; Page 62; 68pp; English.

CC The present sequence is rat G-protein beta 3 subunit. G-protein beta 3 is
CC expressed specifically in taste cells, hence this sequence is referred to
CC as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is
CC involved in the taste transduction pathway. TC-Gbeta3 may be used for
CC identifying taste modulating compounds which can be used in
CC pharmaceutical and food industries to customise taste.
XX Sequence 340 AA;

Query Match 100.0%; Score 1809; DB 21; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.2e-170;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMBOLEKOEALQKQADARACADITLAEVSGLEVGRVQMRRTLRGLAKTYA 60
DB 1 mgemeglkgeaeglkqkqadarkaceditlaelvsgelevgrvmrtrrlrghlaktia 60
QY 61 MHMATDSKLVASASODGKLIWDTYTTNKVHAIPLRSSWVTCAYAFSGFVACGGLDM 120
DB 61 mhmatdskllvasasdgkllwtdytltnkvhaiplrsswmtcayafsgfvaagglidm 120
QY 121 CSTYSLKSRGKVKYSRELISAHGTGLSCCRFLDDNNITVSSGTTTALMDIETGOOKTVE 180
DB 121 csltylskstrgnvkysrelisahgtglscrrfldnnitvssgdtlcalwdletgqkvef 180
QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREGTCQRTTGHESDINAIKCFPPNGEA 240
DB 181 vghgtcdmslavspdyklfissgacdasakimdvregtcqrttghesdinaicffpnea 240
QY 241 ICTGSDASCRFLRADDOELTAYSHESIICGTTVAESLSGRLFAGYDDEPNWWSL 300
DB 241 ictgsdascrlfdradogeltayshesicgittvaselsgrlfaagyddpnwnwds 300
QY 301 KCEVGVLSGHDNRVSCLGVTADGMAVATGWSDFLKIWN 340
DB 301 kcevgvlsghdnrvscilgtadgmavatgwsdfliklwn 340

RESULT 2
AAB15170 ID AAB15170 standard; Protein: 340 AA.
XX AC AAB15170;
XX DT 12-DEC-2000 (first entry)
XX DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #1.
XX KW Rat: Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
XX KM taste transduction pathway; pharmaceutical; food industry; mutation;
XX OS Rattus sp.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT Misc-difference 8 /note="Wild-type Lys substituted by Arg"
XX PN MO200045179-A2.
XX PD 03-AUG-2000.
XX PF 26-JAN-2000; 2000MO-US02218.
XX PR 27-JAN-1999; 99US-0117404.
XX PA (REGC) UNIV CALIFORNIA.

PI Zuker CS, Adler JE, Lindemeier J;
XX WPI; 2000-499361/44.

DR Identifying a compound that modulates sensory signaling in sensory
XX cells for use in pharmaceutical and food industries comprises
XX contacting the compound with a sensory cell specific G-protein beta
XX polypeptide.
XX Disclosure: Page 7; 68pp; English.

CC The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
CC beta 3 is expressed specifically in taste cells, hence this sequence is
CC referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).
CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
CC be used for identifying taste modulating compounds which can be used in
CC pharmaceutical and food industries to customise taste.
CC Note: The present sequence is not shown in the specification but is
CC derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see
CC AAB15168) and information given on page 8 of the disclosure.
XX Sequence 340 AA;

Query Match 99.8%; Score 1806; DB 21; Length 340;
Best Local Similarity 99.7%; Pred. No. 1e-169;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMBOLEKOEALQKQADARACADITLAEVSGLEVGRVQMRRTLRGLAKTYA 60
DB 1 mgemeglkgeaeglkqkqadarkaceditlaelvsgelevgrvmrtrrlrghlaktia 60
QY 61 MHMATDSKLVASASODGKLIWDTYTTNKVHAIPLRSSWVTCAYAFSGFVACGGLDM 120
DB 61 mhmatdskllvasasdgkllwtdytltnkvhaiplrsswmtcayafsgfvaagglidm 120
QY 121 CSTYSLKSRGKVKYSRELISAHGTGLSCCRFLDDNNITVSSGTTTALMDIETGOOKTVE 180
DB 121 csltylskstrgnvkysrelisahgtglscrrfldnnitvssgdtlcalwdletgqkvef 180
QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREGTCQRTTGHESDINAIKCFPPNGEA 240
DB 181 vghgtcdmslavspdyklfissgacdasakimdvregtcqrttghesdinaicffpnea 240
QY 241 ICTGSDASCRFLRADDOELTAYSHESIICGTTVAESLSGRLFAGYDDEPNWWSL 300
DB 241 ictgsdascrlfdradogeltayshesicgittvaselsgrlfaagyddpnwnwds 300
QY 301 KCEVGVLSGHDNRVSCLGVTADGMAVATGWSDFLKIWN 340
DB 301 kcevgvlsghdnrvscilgtadgmavatgwsdfliklwn 340

RESULT 3
AAB15171 ID AAB15171 standard; Protein: 340 AA.
XX AC AAB15171;
XX DT 12-DEC-2000 (first entry)
XX DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #2.
XX KW Rat: Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
XX KM taste transduction pathway; pharmaceutical; food industry; mutation;
XX OS Rattus sp.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT Misc-difference 12 /note="Wild-type Glu substituted by Asp"

XX MO200045179-A2.
 XX 03-AUG-2000.
 XX 26-JAN-2000; 2000WO-US02218.
 XX 27-JAN-1999; 99US-0117404.
 XX (REGC) UNIV CALIFORNIA.
 XX Zuker CS, Adler JE, Lindemeyer J;
 XX WPI; 2000-499361/44.
 XX Identifying a compound that modulates sensory signaling in sensory
 XX cells for use in pharmaceutical and food industries comprises
 XX contacting the compound with a sensory cell specific G-protein beta
 XX polypeptide -
 XX
 XX Disclosure; Page -: 68pp; English.
 XX
 XX The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
 XX beta 3 is expressed specifically in taste cells; hence this sequence is
 XX referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbet3).
 XX TC-Gbet3 is involved in the taste transduction pathway. TC-Gbet3 may
 XX be used for identifying taste modulating compounds which can be used in
 XX pharmaceutical and food industries to customise taste.
 XX Note: The present sequence is not shown in the specification but is
 XX derived from the Rat wild-type TC-Gbet3 sequence given on page 62 (see
 XX AAB15168) and information given on page 8 of the disclosure.
 XX
 XX Sequence 340 AA:
 XX
 XX Query Match 99.8%; Score 1806; DB 21; Length 340;
 XX Best Local Similarity 99.7%; Pred. No. 1e-169; Mismatches 0; Gaps 0;
 XX Matches 339; Conservative 1; Indels 0; Gaps 0;
 QY 1 MGEMEOLKQEAELKQIADARKACADITLAEVSGLEVGVGRVQMRTRRLRGLAKIYA 60
 DB 1 mgemeqlkgeadqlkqjadarkacadiitlaelvsglevgrvqmrtrrlrghlakiya 60
 QY 61 MHWATDSKLIYASASQDGKLIWMDYTTNKVHAIPRSSWMTCAVPSGNFVACGGLNM 120
 DB 61 mhwaidsklliyasasqdgkllwmdytlknkvhairsswmtcayapsgnrtvaacgglndm 120
 QY 121 CSYSLKREGNVKVSRELSAHTGYISCCRFIDNNIVTSQDPTCALMDIETGQKTVF 180
 DB 121 csylslkregnvkvsrelsahtgyisccrfidnnivtsqdtcalwdietgqktvf 180
 QY 181 VGHGTGCKSLAVSPDYKLIIFSGACDASAKIMDVREGTCROTFTGHSDINAIICFPNGEA 240
 DB 181 vghtgckslavspdykllifsgacdasaklmdvregtcrotftghesdinaicffpnea 240
 QY 241 ICTGSDASCRFLDRAQDELFLAVSHESIICGITSVAFSISGRLLFAGYDFNCNWNDSL 300
 DB 241 ictgsdascrflfdradqelflavshesilcgitsvaaisgrlllfagydffncnwds1 300
 QY 301 KCERVGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKINN 340
 DB 301 kcervgvlsghdnrvscclgvtadgmaavatgswdsflkiwn 340
 RESULT 4
 AAB15172
 ID AAB15172 standard; Protein; 340 AA.
 XX
 AC AAB15172;
 XX
 DT 12-DEC-2000 (first entry)
 XX
 DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #3.

XX Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbet3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 KW mutant; mutant.
 XX Rattus sp.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 191 /note= "Wild-type Ala substituted by Gly"
 XX
 XX MO200045179-A2.
 XX 03-AUG-2000.
 XX 26-JAN-2000; 2000WO-US02218.
 XX 27-JAN-1999; 99US-0117404.
 XX (REGC) UNIV CALIFORNIA.
 XX Zuker CS, Adler JE, Lindemeyer J;
 XX WPI; 2000-499361/44.
 XX Identifying a compound that modulates sensory signaling in sensory
 XX cells for use in pharmaceutical and food industries comprises
 XX contacting the compound with a sensory cell specific G-protein beta
 XX polypeptide -
 XX
 XX Disclosure; Page -: 68pp; English.
 XX
 XX The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
 XX beta 3 is expressed specifically in taste cells; hence this sequence is
 XX referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbet3).
 XX TC-Gbet3 is involved in the taste transduction pathway. TC-Gbet3 may
 XX be used for identifying taste modulating compounds which can be used in
 XX pharmaceutical and food industries to customise taste.
 XX Note: The present sequence is not shown in the specification but is
 XX derived from the Rat wild-type TC-Gbet3 sequence given on page 62 (see
 XX AAB15168) and information given on page 8 of the disclosure.
 XX
 XX Sequence 340 AA:
 XX
 XX Query Match 99.8%; Score 1805; DB 21; Length 340;
 XX Best Local Similarity 99.7%; Pred. No. 1.3e-169; Mismatches 1; Gaps 0;
 XX Matches 339; Conservative 0; Indels 0; Gaps 0;
 QY 1 MGEMEOLKQEAELKQIADARKACADITLAEVSGLEVGVGRVQMRTRRLRGLAKIYA 60
 DB 1 mgemeqlkgeadqlkqjadarkacadiitlaelvsglevgrvqmrtrrlrghlakiya 60
 QY 61 MHWATDSKLIYASASQDGKLIWMDYTTNKVHAIPRSSWMTCAVPSGNFVACGGLNM 120
 DB 61 mhwaidsklliyasasqdgkllwmdytlknkvhairsswmtcayapsgnrtvaacgglndm 120
 QY 121 CSYSLKREGNVKVSRELSAHTGYISCCRFIDNNIVTSQDPTCALMDIETGQKTVF 180
 DB 121 csylslkregnvkvsrelsahtgyisccrfidnnivtsqdtcalwdietgqktvf 180
 QY 181 VGHGTGCKSLAVSPDYKLIIFSGACDASAKIMDVREGTCROTFTGHSDINAIICFPNGEA 240
 DB 181 vghtgckslavspdykllifsgacdasaklmdvregtcrotftghesdinaicffpnea 240
 QY 241 ICTGSDASCRFLDRAQDELFLAVSHESIICGITSVAFSISGRLLFAGYDFNCNWNDSL 300
 DB 241 ictgsdascrflfdradqelflavshesilcgitsvaaisgrlllfagydffncnwds1 300
 QY 301 KCERVGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKINN 340
 DB 301 kcervgvlsghdnrvscclgvtadgmaavatgswdsflkiwn 340

RESULT 5

AAW36598

ID AAW36598 standard; Protein; 340 AA.

XX AAW36598;

XX 19-MAY-1998 (first entry)

XX Human G protein beta-3 subunit.

XX G protein beta-3 subunit; variant; mutation; hypertension; diagnosis;
XX cardiovascular disease; metabolic disorder; immunological disorder.

XX Homo sapiens.

XX DE19619362-A1.

XX 20-NOV-1997.

XX 14-MAY-1996; 96DE-1019362.

XX 14-MAY-1996; 96DE-1019362.

XX (BADI) BASF AG.

XX Siftart W;

XX WPI: 1998-000675/01.

XX N-PSDB; AAT96746; AAV09741.

XX Assessing risk of disease, especially hypertension - by detecting
XX mutation in human G-protein beta-3 subunit gene

XX Claim 3; Page 6; 8pp; German.

XX This sequence represents the human G-protein beta 3 subunit. A variant
XX of the gene encoding this protein has applications in the diagnosis of
XX diseases or assessing the risk of a disease associated with G-protein
XX misregulation. G-protein misregulation is associated with hypertension,
XX cardiovascular diseases e.g. coronary heart disease, atherosclerosis,
XX diabetes, stroke and thrombosis, metabolic disorders such as diabetes,
XX diabetic complications, disorders of lipid metabolism and central
XX chemoreception dysfunction (e.g. sudden infant death syndrome), and
XX immunological disorders such as impaired wound healing, tumours, AIDS,
XX cirrhosis and transplant rejection.

SQ Sequence 340 AA;

Query Match 97.4%; Score 1762; DB 19; Length 340;

Best Local Similarity 96.5%; Pred. No. 2.3e-165;

Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEOLEKOEALQKQIADARRACADITLAEVLSGLEVGVGMORTTRTLRGLAKIYA 60
 Db 1 mgemeqlrgeeqkkyiadarracacadvclaelvsglevgrvgtmtrtlrlglnakiya 60
 QY 61 MHNAWTDKLLVSAASQDGLIWDYTTNNVHAIPLRSSVMTCAYAPSGNVACGGIDNM 120
 Db 61 mhwaadskllvsasqgkllwdsytltnkvhalplrssvmwmcayapsgnvvaacggidnm 120
 QY 121 CSYSLKSRGKNGVYRELSAHTGYLSCCRFLDDNNIYTSAGDTTCALMDIETGQKTVF 180
 Db 121 cslynlksrsgnkvyrelsahtgylsccrflddnniivtssgdttcaldwlelvgqktvf 180
 QY 181 VGHGTGCMKSLAVSPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAIQFPNGEA 240
 Db 181 vghtgdcmslavsdpdykflfsgacdasaklmdvregtcrotftghesdinaicfpngea 240
 QY 241 ICTGSDMSAQLFDRADQELTAVSHESIIGTITSVFSLSGRLTAGDOPFCNWNDSL 300
 Db 241 ictgsdmsaqlfdradqelavshesiiigtitsvflsgrltagdopfcnwnwds 300

Db 241 ictgsdmsaqlfdradqelavshesiiigtitsvflsgrltagdopfcnwnwds 300
 QY 301 KCERGVLSGSHDNRYSCGVTADGMAVAATGSMDSFLKTNW 340
 Db 301 keervglisgshdnrysclyvtadgmavatsgwsdflktnw 340

RESULT 6

AAB15169

ID AAB15169 standard; Protein; 340 AA.

XX AAB15169;

XX 12-DEC-2000 (first entry)

XX Human Taste Cell specific G-protein beta 3 subunit.

XX Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
XX taste transduction pathway; pharmaceutical; food industry.

XX Homo sapiens.

XX WO200045179-A2.

XX 03-AUG-2000.

XX 26-JAN-2000; 2000WO-US02218.

XX 27-JAN-1999; 99US-0117404.

XX (REGC) UNIV CALIFORNIA.

XX Zuker CS, Adler JE, Lindemeier J;

XX WPI: 2000-499361/44.

XX N-PSDB; AAA74591.

XX Identifying a compound that modulates sensory signaling in sensory
XX cells for use in pharmaceutical and food industries comprises
XX contacting the compound with a sensory cell specific G-protein beta
XX polypeptide -

XX Claim 1; Page 63; 68pp; English.

XX The present sequence is human G-protein beta 3 subunit. G-protein beta 3
XX is expressed specifically in taste cells, hence this sequence is referred
XX to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3
XX is involved in the taste transduction pathway. TC-Gbeta3 may be used for
XX identifying taste modulating compounds which can be used in
XX pharmaceutical and food industries to customise taste.

SQ Sequence 340 AA;

Query Match 97.4%; Score 1762; DB 21; Length 340;

Best Local Similarity 96.5%; Pred. No. 2.3e-165;

Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEOLEKOEALQKQIADARRACADITLAEVLSGLEVGVGMORTTRTLRGLAKIYA 60
 Db 1 mgemeqlrgeeqkkyiadarracacadvclaelvsglevgrvgtmtrtlrlglnakiya 60
 QY 61 MHNAWTDKLLVSAASQDGLIWDYTTNNVHAIPLRSSVMTCAYAPSGNVACGGIDNM 120
 Db 61 mhwaadskllvsasqgkllwdsytltnkvhalplrssvmwmcayapsgnvvaacggidnm 120
 QY 121 CSYSLKSRGKNGVYRELSAHTGYLSCCRFLDDNNIYTSAGDTTCALMDIETGQKTVF 180
 Db 121 cslynlksrsgnkvyrelsahtgylsccrflddnniivtssgdttcaldwlelvgqktvf 180
 QY 181 VGHGTGCMKSLAVSPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAIQFPNGEA 240
 Db 181 vghtgdcmslavsdpdykflfsgacdasaklmdvregtcrotftghesdinaicfpngea 240
 QY 241 ICTGSDMSAQLFDRADQELTAVSHESIIGTITSVFSLSGRLTAGDOPFCNWNDSL 300
 Db 241 ictgsdmsaqlfdradqelavshesiiigtitsvflsgrltagdopfcnwnwds 300

QY 241 ICTGSDASCRFLPDLRADDELTAAYSHESITCGITVAFSISGRLLFAGYDDFNCNVWDSL 300
 DB 241 Ictgsdascrlldlradeqelcfsheisllcgltsvaflsgrllfagydlnncnvwdsm 300
 QY 301 KCERVGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIMN 340
 DB 301 kservgllsgndrvsclygtadgmavatsgwsdflkilm 340
 RESULT 7
 AAY67865 standard; protein; 340 AA.
 ID AAY67865;
 AC AAY67865;
 DT 25-APR-2000 (first entry)
 DE Human Hgb3 G-protein beta3 subunit amino acid sequence.
 DE Human Hgb3 G-protein beta3 subunit amino acid sequence.
 DE Ste20p/PAK; G-protein-coupled receptor signal transduction; human; Hgb3;
 DE Ste4p/Gbeta interaction domain; p21-activated protein kinase;
 DE G-protein coupled receptor signal transduction;
 OS Homo sapiens.
 PA (LEBERER) LEBERER E.
 PA (LEBERER) LEBERER E.
 PA (THOMAS) THOMAS D Y.
 PA (WHIT) WHITNEY M.
 PI Leberer E, Leeuw T, Thomas DY, Whiteway M;
 WP; 2000-137553/13.
 DR Interacting polypeptides involved in G-protein-coupled receptor signal
 PT transduction -
 PS Claim 3; Fig 6; 91pp; English.
 CC This sequence represents the beta3 subunit of a human G-protein. The
 CC invention relates to the G-protein beta subunit interaction domain of the
 CC Ste20p/PAK family of protein kinases. The Ste20p/PAK family of protein
 CC kinases are p21-activated protein kinases (PAK) and they are involved in
 CC many varied cellular processes ranging from morphogenesis and stress
 CC response, to apoptosis. Interacting polypeptides Ste4p/Gbeta and
 CC Ste20p/PAK are useful for designing in vitro and in vivo experimental
 CC models which enable the screening of large collections of synthetic,
 CC semi-synthetic, or natural compounds for therapeutic use in Ste4p/Gbeta
 CC and Ste20p/PAK dependent diseases.
 SQ Sequence 340 AA;
 Query Match 97.4%; Score 1762; DB 21; Length 340;
 Best Local Similarity 96.5%; Pred. No. 2.3e-165;
 Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MGEEOQLKOEAEOLKQIADARRACADITLAEVSGLEAVGVORRTRETLGHLAKIYA 60
 DB 1 mgemeqlqgeaeqlkqjadarkacadvltlaevsgleavgyvqmrtrrtllrghlakia 60
 QY 61 MHWATDSKLIVASQDGLIYMDTYTNKVAHPIERSSWMTCAVAPSSNEFAACGGLNM 120
 DB 61 mhwatdskllyvasqdgkilywdsyttnkvhahpirtswwmtcavapsnfnfaacgglnm 120

QY 121 CSTSLKSRREGNVKVSRELTAHTGYLSCCRFLDNNITWSSGPTCALMDIETGOQTVF 180
 DB 121 cstslksrregnvkvsreltahtgylsccrflldnnitwssgptcalmdietgoqtvf 180
 QY 181 VGHTRDCKSLANSPDYKFLTSGACDASAKIMDVRETCRQFTFHESDINAIQFFPNGEA 240
 DB 181 vghtrdckslanspdykfltsagcdasakimdvretrcrqftfhesdinalqffpnea 240
 QY 241 ICTGSDASCRFLPDLRADDELTAAYSHESITCGITVAFSISGRLLFAGYDDFNCNVWDSL 300
 DB 241 Ictgsdascrlldlradeqelcfsheisllcgltsvaflsgrllfagydlnncnvwdsm 300
 QY 301 KCERVGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIMN 340
 DB 301 kservgllsgndrvsclygtadgmavatsgwsdflkilm 340
 RESULT 8
 AAB15173 standard; protein; 340 AA.
 ID AAB15173;
 AC AAB15173;
 DT 12-DEC-2000 (first entry)
 DE Mutant human Taste Cell specific G-protein beta 3 subunit variant #1.
 DE Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 DE Taste transduction pathway; pharmaceutical; food industry; mutation;
 DE muteln; mutant.
 OS Homo sapiens.
 OS Synthetic.
 PH Key location/Qualifiers
 FT Misc-difference 7 /note="Wild-type Leu substituted by Ile"
 FT WO200045179-A2.
 XX 03-AUG-2000.
 XX 26-JAN-2000; 2000WO-US02218.
 XX 27-JAN-1999; 99US-0117404.
 XX (REGC) UNITV CALIFORNIA.
 XX Zuker CS, Adler JE, Lindemeyer J;
 WP; 2000-499361/44.
 DR Identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -
 PS Disclosure; page 7; 66pp; English.
 CC The present sequence is a mutant human G-protein beta 3 subunit.
 CC G-protein beta 3 is expressed specifically in taste cells, hence this
 CC sequence is referred to as Taste Cell specific G-protein beta 3 subunit
 CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
 CC TC-Gbeta3 may be used for identifying taste modulating compounds which
 CC can be used in pharmaceutical and food industries to customize taste.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type TC-Gbeta3 sequence given on page 63
 CC (see AAB15169) and information given on page 8 of the disclosure.
 SQ Sequence 340 AA;

Query Match 97.3%; Score 1760; DB 21; Length 340;
 Best Local Similarity 96.2%; Pred. No. 3,56-165;
 Matches 327; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEHQLKQAEOLKQIADARACADITLAEVSGLEVGRVOMRTTRRLRGHLAKIYA 60
 DB 1 mgeheqlrgeaeqlkqiadarkacadvlaelvsgelevgrvmrtrrrlrghlakiya 60
 QY 61 MHWATDSKLLVASASODGKLIWDTYTTNKVHAIPLRSSWMTCAYPAGNFVACGGLDM 120
 DB 61 mhwatdskllvasasdgkllwdsytltnkvhaiplrsswmtcaypagnfvaacggladm 120
 QY 121 CSTYSLKSRGNKVKYSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGOOKTVF 180
 DB 121 cstynlksregnvkysrelsahtgylsccrflddnnivtssgdttcaldietgqkctvf 180
 QY 181 VGHTEGMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACFPNGEA 240
 DB 181 vghtegmslavspdyklfiscgadcasaklmdvregtcrotftghesdinaicfpngea 240
 QY 241 ICTGSDASCRFLRADQELTAVSHESIICGTTVAEFLSGRLFAGYDPCNWNWDSL 300
 DB 241 ictgsdascrflradqelictshesilcgltvaelsgrllfagyddpcnwnwds 300
 QY 301 KCEYGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIKWN 340
 DB 301 kceygvlsghdnrvsclgvtadgmavatgswdsflkikwn 340

RESULT 9
 AAB15174
 ID AAB15174 standard; Protein: 340 AA.
 AC AAB15174;
 DE 12-DEC-2000 (first entry)
 DE Mutant human Taste Cell specific G-protein beta 3 subunit variant #2.
 KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 OS Homo sapiens.
 OS Synthetic.
 FT Key Location/Qualifiers
 FT Misc-difference 161 /note= "Wild-type Ser substituted by Thr"
 PN W0200045179-A2.
 PD 03-AUG-2000.
 PF 26-JAN-2000; 2000MO-US02218.
 PR 27-JAN-1999; 99US-0117404.
 PA (REGC) UNIV CALIFORNIA.
 PI Zuker CS, Adler JE, Lindemeyer J;
 DR WPI: 2000-499361/44.
 PT Identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PS polypeptide -
 PS Disclosure: Page - 7: 66pp; English.
 CC The present sequence is a mutant human G-protein beta 3 subunit.
 CC G-protein beta 3 is expressed specifically in taste cells, hence this

CC sequence is referred to as Taste Cell specific G-protein beta 3 subunit
 CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
 CC TC-Gbeta3 may be used for identifying taste modulating compounds which
 CC can be used in pharmaceutical and food industries to customize taste.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type TC-Gbeta3 sequence given on page 63
 CC (see AAB15169) and information given on page 8 of the disclosure.
 SQ Sequence 340 AA;

Query Match 97.2%; Score 1759; DB 21; Length 340;
 Best Local Similarity 96.2%; Pred. No. 4,4e-165;
 Matches 327; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEHQLKQAEOLKQIADARACADITLAEVSGLEVGRVOMRTTRRLRGHLAKIYA 60
 DB 1 mgeheqlrgeaeqlkqiadarkacadvlaelvsgelevgrvmrtrrrlrghlakiya 60
 QY 61 MHWATDSKLLVASASODGKLIWDTYTTNKVHAIPLRSSWMTCAYPAGNFVACGGLDM 120
 DB 61 mhwatdskllvasasdgkllwdsytltnkvhaiplrsswmtcaypagnfvaacggladm 120
 QY 121 CSTYSLKSRGNKVKYSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGOOKTVF 180
 DB 121 cstynlksregnvkysrelsahtgylsccrflddnnivtssgdttcaldietgqkctvf 180
 QY 181 VGHTEGMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACFPNGEA 240
 DB 181 vghtegmslavspdyklfiscgadcasaklmdvregtcrotftghesdinaicfpngea 240
 QY 241 ICTGSDASCRFLRADQELTAVSHESIICGTTVAEFLSGRLFAGYDPCNWNWDSL 300
 DB 241 ictgsdascrflradqelictshesilcgltvaelsgrllfagyddpcnwnwds 300
 QY 301 KCEYGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIKWN 340
 DB 301 kceygvlsghdnrvsclgvtadgmavatgswdsflkikwn 340

RESULT 10
 AAB15175
 ID AAB15175 standard; Protein: 340 AA.
 AC AAB15175;
 DE 12-DEC-2000 (first entry)
 DE Mutant human Taste Cell specific G-protein beta 3 subunit variant #3.
 KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 OS Homo sapiens.
 OS Synthetic.
 FT Key Location/Qualifiers
 FT Misc-difference 301 /note= "Wild-type Lys substituted by Arg"
 PN W0200045179-A2.
 PD 03-AUG-2000.
 PF 26-JAN-2000; 2000MO-US02218.
 PR 27-JAN-1999; 99US-0117404.
 PA (REGC) UNIV CALIFORNIA.
 PI Zuker CS, Adler JE, Lindemeyer J;

DR WPI: 2000-499361/44.

XX Identifying a compound that modulates sensory signaling in sensory
PT cells for use in pharmaceutical and food industries comprises
PT contacting the compound with a sensory cell specific G-protein beta
PT polypeptide.

PS Disclosure: Page -: 68pp; English.

XX The present sequence is a mutant human G-protein beta 3 subunit.
CC G-protein beta 3 is expressed specifically in taste cells, hence this
CC sequence is referred to as Taste Cell specific G-protein beta 3 subunit
CC (TC-Gbetas). TC-Gbetas is involved in the taste transduction pathway.
CC TC-Gbetas may be used for identifying taste modulating compounds which
CC can be used in pharmaceutical and food industries to customize taste.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type TC-Gbetas3 sequence given on page 63
CC (see AAB15169) and information given on page 8 of the disclosure.

CC Sequence 340 AA;

Query Match 97.2%; Score 1759; DB 21; Length 340;
Best Local Similarity 96.2%; Pred. No. 4.4e-165;
Matches 327; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

OY 1 MGEMQOLKOEAEQKQIADARKACADITLAEVSGLEVGRVQMTTRTLRGLAKIYA 60
DB 1 mgemeqlrgeaeqllkqgladarkacadvrlaelvsglevgrvqmttrtlrlghlakiya 60
OY 61 MHMATDSKILVASODGKLIYDITTTNNKVAIPLRSSWMTCAVAPSGNFVACGGLDMM 120
DB 61 mhmatdskilvasodgkliyditttnkvaiplrsswmtcavapsngnfvacggldmm 120
OY 121 CSISYLSKREGNVKVSRELSAHTGYLSCRFIDNNIVTSSGDTTCALMDIETGQKTVF 180
DB 121 csisylskregnvksrelsahtgylsccrfidnnivtssgdttcaldietgqktvf 180
OY 181 VGHGTGDCMSILAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
DB 181 vghgtgdcmsilavspdyklfisgacdasaklmdvregtcrotftghesdinaiictfpngea 240
OY 241 ICTGSDDASCRLEFDLRADDELTAIVSHESITIGITVAFSLGRILFAGYDDPNCNWMDSL 300
DB 241 ictgsddascrlefdlraddelictfshesitigivafslsgrilfagyddpncnwmdsl 300
OY 301 KCEKRVGLSGHDNRVSCLGVTADGMAVATGSMDSFLKIWN 340
DB 301 kcervglsghdnrvsclgvtadgmaavatgsmwsdflkiwn 340

RESULT 11

AAR85859 standard; peptide; 340 AA.

AC AAR85859;

DI 13-SEP-1996 (first entry)

DE WD-40 domain-contg. bovine G-beta-1 protein.

KW WD40 repeat region; beta-transducin; protein-protein interaction; drug;
KW intracellular signalling; protein kinase C; homology; motif; modulator;
KW receptors of activated protein kinase; enzyme activity; isozyme; human.

OS Bos taurus.

PN WO9521252-A2.

XX 10-AUG-1995.

PF 31-JAN-1995; 95WO-US01210.

PR 01-FEB-1994; 94US-0190802.

PA (STRD) UNIT LELAND STANFORD JUNIOR.

PI Mochly-Rosen D, Ron D;

DR WPI: 1995-283772/37.

PT New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
PT activity of a protein, eg. protein kinase C, which interacts with a
PT protein contg. a WD-40 region.

PS Example 5; Page 102-103; 351pp; English.

XX Proteins AAR8551-92 are protein which contain at least one WD-40 (also
CC called beta-transducin homologous) amino acid repeat motifs. The WD-40
CC regions are involved in protein-protein interactions between proteins
CC involved in intracellular signalling. An example of such an interaction
CC is between protein kinase C and receptors of activated protein kinase
CC (RACK), esp. RACK-1 (AAR85850). Proteins AAR8551-82 were isolated based
CC on homology with beta-transducin, whereas proteins AAR8582-92 were
CC isolated based on homology with the WD-40 consensus sequence (AAR85933).
CC The proteins were used to construct the peptides AAR84928-R85063 and
CC AAR85786-R85842. The peptides can be used to identify target proteins
CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
CC proteins involved in protein-protein interaction and to screen for drugs
CC that will affect protein-protein interaction involving WD-40 domains.

XX Sequence 340 AA;

Query Match 87.0%; Score 1573; DB 16; Length 340;
Best Local Similarity 83.2%; Pred. No. 9.6e-147;
Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;

OY 1 MGEMQOLKOEAEQKQIADARKACADITLAEVSGLEVGRVQMTTRTLRGLAKIYA 60
DB 1 mgemeqlrgeaeqllkqgladarkacadvrlaelvsglevgrvqmttrtlrlghlakiya 60
OY 61 MHMATDSKILVASODGKLIYDITTTNNKVAIPLRSSWMTCAVAPSGNFVACGGLDMM 120
DB 61 mhmatdskilvasodgkliyditttnkvaiplrsswmtcavapsngnfvacggldmm 120
OY 121 CSISYLSKREGNVKVSRELSAHTGYLSCRFIDNNIVTSSGDTTCALMDIETGQKTVF 180
DB 121 csisylskregnvksrelsahtgylsccrfidnnivtssgdttcaldietgqktvf 180
OY 181 VGHGTGDCMSILAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
DB 181 vghgtgdcmsilavspdyklfisgacdasaklmdvregtcrotftghesdinaiictfpngea 240
OY 241 ICTGSDDASCRLEFDLRADDELTAIVSHESITIGITVAFSLGRILFAGYDDPNCNWMDSL 300
DB 241 ictgsddascrlefdlraddelictfshesitigivafslsgrilfagyddpncnwmdsl 300
OY 301 KCEKRVGLSGHDNRVSCLGVTADGMAVATGSMDSFLKIWN 340
DB 301 kcervglsghdnrvsclgvtadgmaavatgsmwsdflkiwn 340

RESULT 12

AAV67863 standard; protein; 340 AA.

AC AAV67863;

DI 25-APR-2000 (first entry)

DE Human Hgb1 G-protein beta1 subunit amino acid sequence.

KW Ste20p/PAK; G-protein-coupled receptor signal transduction; human; Hgb1;
KW Ste4p/Gbeta interaction domain; p21-activated protein kinase;
KW G-protein coupled receptor signal transduction;

XX Homo sapiens.
 OS CA2219958-A1.
 PN 07-JUL-1999.
 PD 07-JAN-1998: 98CA-2219958.
 PF 07-JAN-1998: 98CA-2219958.
 PR 07-JAN-1998: 98CA-2219958.
 XX
 XX (LEBE/) LEBERER E.
 PA (LEBU/) LEBERER E.
 PA (THOM/) THOMAS D Y.
 PA (WHIT/) WHITEMAN M.
 XX
 PI Leberer E, Leeuw T, Thomas DY, Whiteway M;
 DR WPI; 2000-137553/13.
 XX
 PT Interacting polypeptides involved in G-protein-coupled receptor signal
 PT transduction -
 XX
 PS Claim 3; Fig 6; 91pp: English.
 XX
 CC This sequence represents the beta subunit of a human G-protein. The
 CC invention relates to the G-protein beta subunit interaction domain of the
 CC Ste20p/PAK family of protein kinases. The Ste20p/PAK family of protein
 CC kinases are p21-activated protein kinases (PAK), and they are involved in
 CC many varied cellular processes ranging from morphogenesis and stress
 CC response, to apoptosis. Interacting polypeptides Ste4p/Cbeta and
 CC Ste20p/PAK are useful for designing in vitro and in vivo experimental
 CC models which enable the screening of large collections of synthetic,
 CC semi-synthetic, or natural compounds for therapeutic use in Ste4p/Cbeta
 CC and Ste20p/PAK dependent diseases.
 CC
 SQ Sequence 340 AA;

Query Match 87.0%; Score 1573; DB 21; Length 340;
 Best Local Similarity 83.2%; Pred. No. 9, 6e-147;
 Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;
 QY 1 MGEMDLKQEAQKQIDARKKACADITLAEVSGLEVGVRVOMTRRTIRGLAKIYA 60
 DB 1 mselldqlrgeaeqllngirdarkacacatlsgltlnldpvgirlqmrtrtlrghlaxiya 60
 QY 61 MHVATSKLLVASQDGLIWDITTTNKVHAIPLRSSVWMTCAVAPSGNVAAGGLDM 120
 DB 61 mhvgtdsrllvasaqqkllwdsytltnkvhaplrssvwmctayapsngnvaagglidni 120
 QY 121 CSYLSKREGNVAKRSRLSAHTGYLSCCRFLDNNIYSSGDTTCALMDIETGOQKTVF 180
 DB 121 csylntkrtregnvarelaghgyisccrflldnglvyssgdtlcalwdietgqqltf 180
 QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFTGHESDINAICTFPNGEA 240
 DB 181 lghtgdcmslslapdtrrlfvsagcdasaklwdvregmctqftfghesdlnaictfpgnga 240
 QY 241 ICTGSDASCRFLRADQELTAISHESIICGITSVAFLSGRLLFAGYDDFNCAVWDSL 300
 DB 241 fctgsddatcrflfdradqelmtysndnllcgltsvsfksgrlllagyddfnncvwdsl 300
 QY 301 KCERGVLSGHDNRVSCGLVTAADGMAVATGSDSFLKIMN 340
 DB 301 kdragvlsghdnrvscglvtdgmaavatsvdsflkwn 340

RESULT 13
 AAR85863
 ID AAR85863 standard; peptide: 340 AA.
 XX
 AC AAR85863;

XX 13-SEP-1996 (first entry)
 DT WD-40 domain-contg. human G-beta-2 protein.
 DE WD40 repeat region; beta-transducin; protein-protein interaction; drug;
 KW intracellular signalling; protein kinase C; homology; motif; modulator;
 KW receptors of activated protein kinase; enzyme activity; isozyme; human.
 XX
 OS Homo sapiens.
 XX
 PN W09521252-A2.
 XX
 PD 10-AUG-1995.
 PF 31-JAN-1995; 95WO-US01210.
 XX
 PR 01-FEB-1994; 94US-0190802.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Mochly-Rosen D, Ron D;
 DR WPI; 1995-283772/37.
 XX
 PT New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
 PT activity of a protein, eg. protein kinase C, which interacts with a
 PT protein contg. a WD-40 region.
 XX
 PS Example 5; Page 109-110; 351pp: English.
 XX
 CC Proteins AAR8581-92 are protein which contain at least one WD-40 (also
 CC called beta-transducin homologous) amino acid repeat motifs. The WD-40
 CC regions are involved in protein-protein interactions between proteins
 CC involved in intracellular signalling. An example of such an interaction
 CC is between protein kinase C and receptors of activated protein kinase
 CC (RACK), esp. RACK-1 (AAR85850). Proteins AAR8581-82 were isolated based
 CC on homology with beta-transducin, whereas proteins AAR8582-92 were
 CC isolated based on homology with the WD-40 consensus sequence (AAR85893).
 CC The proteins were used to construct the peptides AAR84928-R85063 and
 CC AAR85786-R85842. The peptides can be used to identify target proteins
 CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
 CC proteins involved in protein-protein interaction and to screen for drugs
 CC that will affect protein-protein interaction involving WD-40 domains.
 CC
 SQ Sequence 340 AA;

Query Match 84.2%; Score 1523; DB 16; Length 340;
 Best Local Similarity 80.9%; Pred. No. 8, 1e-142;
 Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;
 QY 1 MGEMDLKQEAQKQIDARKKACADITLAEVSGLEVGVRVOMTRRTIRGLAKIYA 60
 DB 1 mselldqlrgeaeqllngirdarkacacatlsgltlnldpvgirlqmrtrtlrghlaxiya 60
 QY 61 MHVATSKLLVASQDGLIWDITTTNKVHAIPLRSSVWMTCAVAPSGNVAAGGLDM 120
 DB 61 mhvgtdsrllvasaqqkllwdsytltnkvhaplrssvwmctayapsngnvaagglidni 120
 QY 121 CSYLSKREGNVAKRSRLSAHTGYLSCCRFLDNNIYSSGDTTCALMDIETGOQKTVF 180
 DB 121 csylntkrtregnvarelaghgyisccrflldnglvyssgdtlcalwdietgqqltf 180
 QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFTGHESDINAICTFPNGEA 240
 DB 181 aghsdgmsslslapdtrrlfvsagcdasaklwdvxdmrcgrqftfghesdlnavafpnga 240
 QY 241 ICTGSDASCRFLRADQELTAISHESIICGITSVAFLSGRLLFAGYDDFNCAVWDSL 300
 DB 241 fctgsddatcrflfdradqelmtysndnllcgltsvafsfgrlllagyddfnncvwdsl 300
 QY 301 KCERGVLSGHDNRVSCGLVTAADGMAVATGSDSFLKIMN 340

Db 301 kgdravlaghndrvsclygtddgmavatswdsfklkm 340

RESULT 14
AAV67864
ID AAV67864 standard; protein; 340 AA.
XX
AC AAV67864;
XX
DT 25-APR-2000 (first entry)
XX
DE Human Hgb2 G-protein beta2 subunit amino acid sequence.
XX
KW Ste20p/PAK: G-protein-coupled receptor signal transduction; human; Hgb2;
KM Ste4p/beta interaction domain; p21-activated protein kinase;
KW G-protein coupled receptor signal transduction;
XX
OS Homo sapiens.
XX
PN CA2219958-A1.
XX
PD 07-JUL-1999.
XX
PF 07-JAN-1998; 98CA-2219958.
XX
PR 07-JAN-1998; 98CA-2219958.
XX
PA (LEBERER) LEBERER E.
PA (LEEUW) LEEUW T.
PA (THOMAS) THOMAS D Y.
PA (WHIT) WHITEWAY M.
XX
PI Leberer E, Leeuw T, Thomas DY, Whiteway M;
XX
DR WPI; 2000-137553/13.
XX
PT Interacting polypeptides involved in G-protein-coupled receptor signal
XX transduction -
XX
PS Claim 3; Fig 6; 91pp; English.
XX
CC This sequence represents the beta2 subunit of a human G-protein. The
CC invention relates to the G-protein beta subunit interaction domain of the
CC Ste20p/PAK family of protein kinases. The Ste20p/PAK family of protein
CC kinases are p21-activated protein kinases (PAK), and they are involved in
CC many varied cellular processes ranging from morphogenesis and stress
CC response, to apoptosis. Interacting polypeptides Ste4p/beta and
CC Ste20p/PAK are useful for designing in vitro and in vivo experimental
CC models which enable the screening of large collections of synthetic,
CC semi-synthetic, or natural compounds for therapeutic use in Ste4p/Gbeta
CC and Ste20p/PAK dependent diseases.
XX
SQ Sequence 340 AA;

Query Match 84.2%; Score 1523; DB 21; Length 340;
Best Local Similarity 80.9%; Pred. No. 8.1e-142;
Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGEHOLKOEAEOLKQIADARACADITLAEVSGLEVYGRVOMRRRLRHLAKIYA 60
DB 1 mselqelrgeaeqlnqldardkacgstltqtagldpvgtrttrtlrghlakiya 60
QY 61 MHWATDSKLVASADGKLIWMDTYTNNKVAIPLRSSWMTCAVAPSGNFVACGGLDMN 120
DB 61 mhwatdsrllvasagdkllwdsytlmkvhaiprswmtcayapsnfrvaagglndi 120
QY 121 CSITSLSKREGNNKVSRELTAHTGYLSCCFELDDNNIVTSSGDTTCALMDITFGQOKTVF 180
DB 121 csitslktregnnvrsrelphtgylscctfiddnqiltsqdtcalwdietgqtvfi 180
QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKILMDVRECTGKOTFTGHSIDINAICFPNPGA 240

Db 181 aghsgdwmsislpadgrltfvsagcdasiklwdyrdsmcrtfignesdlnvaffpnja 240

QY 241 ICTGSDASCRLFDLRADDELTFVSHESIICGFTSVAPSLGRLLFAGYDDPNCNVWDSL 300
DB 241 ftgsddatcrlfdlradeqllmshndilcgltsvatsrgllllygyddfnclnwdam 300

QY 301 KCERGVLSGHDNRVSCLVYADGMAVATGSWDSFLKIWN 340
DB 301 kgdravlaghndrvsclygtddgmavatswdsfklkm 340

RESULT 15
AAW59364
ID AAW59364 standard; Protein; 299 AA.
XX
AC AAW59364;
XX
DT 10-SEP-1998 (first entry)
XX
DE Human G-protein beta-3 subunit protein.
XX
KW G protein; beta-3 subunit; human; hypertension; immunodeficient; stroke;
KM treatment; cardiovascular disease; metabolic disorder; tumour metastasis;
KM coronary heart disease; post-angioplastic re-stenosis; diabetes;
KM nephropathy; polynuropathy; retinopathy.
XX
OS Homo sapiens.
XX
PN W09811212-A1.
XX
PD 19-MAR-1998.
XX
PF 29-AUG-1997; 97MO-EP04709.
XX
PR 13-SEP-1996; 96DE-1037518.
XX
PA (SIFERT) SIFERT W.
XX
PI Siefert W;
XX
DR WPI; 1998-271665/24.
DR N-PSDB; AAV34857.
XX
PT Variant of human G protein beta-3 sub-unit - associated with
XX hypertension
XX
PS Claim 2; Page 12-13; 34pp; German.
XX
CC This sequence represents a human G-protein beta-3 subunit consisting
CC of up to six WD repeat motifs (as found in hypertensive subjects, rather
CC than the seven WD repeat motifs found in normotensive subjects). The
CC nucleic acid sequence encoding this protein can be expressed in a host
CC organism to produce the protein, preferably where the host organism is an
CC immunodeficient person, especially an HIV-positive person. This sequence
CC can be used to prepare a medicament for treating diseases associated with
CC G protein mis-control e.g. cardiovascular disease, metabolic disorders or
CC post-angioplastic re-stenosis, hypertension, coronary heart disease, stroke,
CC polynuropathy or retinopathy) or tumour metastasis.
XX
SQ Sequence 299 AA;

Query Match 84.1%; Score 1520.5; DB 19; Length 299;
Best Local Similarity 85.0%; Pred. No. 1.2e-141;
Matches 289; Conservative 7; Mismatches 3; Indels 41; Gaps 1;

QY 1 MGEHOLKOEAEOLKQIADARACADITLAEVSGLEVYGRVOMRRRLRHLAKIYA 60
DB 1 mgemeqlrgeaeqlkxjadarkacadvclaelvsglevygrvqmrtrtlrghlakiya 60
QY 61 MHWATDSKLVASADGKLIWMDTYTNNKVAIPLRSSWMTCAVAPSGNFVACGGLDMN 120

Fri Sep 28 10:45:04 2001

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Page 10

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Db 61 mhwatdsckllvsasqdkllvwdsytlmkvhaipirsswmlcayapsgnlvaccgldnm 120
QY 121 CSYISLKSREGANKVARELSAHTGYLSCCRFDNNINVTSSGDTTCALMDIETGOQKTVF 180
Db 121 cslynlksregnvkvstelsahcylascrfiddmniivssgdtc----- 166
QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKIMDYREGTCROTFTGHESDINAI CFPNGEA 240
Db 167 -----aklwdvregtcrqtlitghesdinaicifpnea 199
QY 241 ICTGSDDASCRLFDLRADQELTAVSHESITCGITSVAFSLSGRLFAGYDPCNVMWDSL 300
Db 200 ictgsddascrlfqlradqelictsheslcyllsvafslsgrllfagyddfcncvwds 259
QY 301 KCERYGVLSGHDNRVSCIGYVADGMAVATGSMDSFLKIMN 340
Db 260 keervgllsghdnrsvsclyvradgmavatlgs wdsflkiwn 299
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Search completed: September 28, 2001, 10:29:21
Job time: 71 sec

OM protein - protein search, 10:28:09 ; Search time 20.71 Seconds
Run on: September 28, 2001, (without alignments)
338.036 Million cell updates/second

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                  Maximum Match 100%

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Listing first 45 summaries

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Database : Issued Patents_AA.*
1: /cgn2.6/prodata/2/1aa/5A.COMB.pep.*
2: /cgn2.6/prodata/2/1aa/5B.COMB.pep.*
3: /cgn2.6/prodata/2/1aa/6A.COMB.pep.*
4: /cgn2.6/prodata/2/1aa/6B.COMB.pep.*
5: /cgn2.6/prodata/2/1aa/PCrUS.COMB.pep.*
6: /cgn2.6/prodata/2/1aa/backfiles1.pep.*
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pred. No. is the number of results predicted by chance by a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1762	87.4	340	4	US-09-180-783-2	Sequence 2, Appl
2	1573	87.0	340	4	US-08-190-802A-38	Sequence 38, Appl
3	1523	88.2	340	4	US-08-190-802A-42	Sequence 42, Appl
4	1520.5	88.1	299	4	US-09-147-826B-2	Sequence 2, Appl
5	1467	81.1	341	1	US-08-190-802A-45	Sequence 45, Appl
6	1452	80.4	340	1	US-08-190-802A-40	Sequence 40, Appl
7	1419	78.3	326	1	US-08-190-802A-39	Sequence 39, Appl
8	946.5	35.3	395	3	US-09-032-372-1	Sequence 1, Appl
9	639	32.3	423	3	US-08-190-802A-61	Sequence 61, Appl
10	297.5	16.4	317	1	US-08-190-802A-27	Sequence 27, Appl
11	297.5	16.4	317	1	US-08-190-802A-41	Sequence 41, Appl
12	297.5	16.4	317	1	US-08-190-802A-47	Sequence 47, Appl
13	295	16.3	704	1	US-08-190-802A-62	Sequence 62, Appl
14	295	16.3	704	1	US-08-188-582-5	Sequence 5, Appl
15	295	16.3	704	1	US-08-646-715-5	Sequence 5, Appl
16	295	16.3	704	2	US-08-308-818-3	Sequence 3, Appl
17	284	15.7	587	3	US-08-899-578-2	Sequence 2, Appl
18	275.5	15.2	704	1	US-08-188-582-18	Sequence 18, Appl
19	275.5	15.2	704	1	US-08-646-715-18	Sequence 18, Appl
20	263.5	14.6	439	1	US-08-190-802A-65	Sequence 65, Appl
21	263.5	14.6	798	1	US-08-190-802A-64	Sequence 64, Appl
22	263.5	14.6	798	2	US-08-190-802A-68	Sequence 68, Appl
23	263.5	14.6	798	2	US-08-308-818-2	Sequence 2, Appl
24	261.5	14.5	318	1	US-08-190-802A-33	Sequence 33, Appl
25	261.5	14.5	514	1	US-08-190-802A-66	Sequence 66, Appl
26	252.5	14.0	713	1	US-08-190-802A-63	Sequence 63, Appl
27	242.5	13.4	343	4	US-09-063-743-5	Sequence 5, Appl

28	240	13.3	305	3	US-08-965-600-1	Sequence 1, April
29	240	13.3	375	4	US-09-063-743-1	Sequence 1, April
30	235	13.0	409	2	US-08-283-917-3	Sequence 3, April
31	235	13.0	409	2	US-08-961-716-3	Sequence 3, April
32	235	13.0	410	2	US-08-283-917-9	Sequence 9, April
33	235	13.0	410	2	US-08-961-716-9	Sequence 9, April
34	235	13.0	409	1	US-08-190-802A-51	Sequence 51, April
35	225.5	12.5	409	1	US-08-190-802A-30	Sequence 30, April
36	217	12.0	517	1	US-08-130-802A-70	Sequence 31, April
37	216.3	12.0	906	1	US-08-130-802A-31	Sequence 31, April
38	216.3	11.7	2627	2	US-08-751-189-3	Sequence 3, April
39	211.5	11.7	2627	2	US-09-060-836-3	Sequence 3, April
40	211.5	11.7	2627	2	US-09-184-445-3	Sequence 3, April
41	211.5	11.7	2629	2	US-08-751-189-4	Sequence 4, April
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43	199.5	11.0	376	2	US-09-184-534-5	Sequence 4, April
44	199.5	11.0	376	2	US-08-883-534-5	Sequence 5, April
45	197.5	10.9	422	1	US-09-204-764-5	Sequence 5, April
					US-08-190-802A-52	Sequence 52, April

ALIGNMENTS

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Query Match	Best Local Similarity	97.4%: Score 1762; DB 4: length 340;
Matches 328; Conservative	96.5%: Pred. No. 5, 9e-173; Mismatches 4; Indels 0; Gaps 0	
1 MGEMEOLKQEAEOALKQIADARKACADITLAEIVSGLEEVGRVOMTRRTLLGHAKIYYA 60	1 MGEMEOLKQEAEOALKQIADARKACADITLAEIVSGLEEVGRVOMTRRTLLGHAKIYYA 60	
2Y 1 MGEMEOLKQEAEOALKQIADARKACADITLAEIVSGLEEVGRVOMTRRTLLGHAKIYYA 60	1 MGEMEOLKQEAEOALKQIADARKACADITLAEIVSGLEEVGRVOMTRRTLLGHAKIYYA 60	
Db 1 MGEMEOLKQEAEOALKQIADARKACADITLAEIVSGLEEVGRVOMTRRTLLGHAKIYYA 120	1 MGEMEOLKQEAEOALKQIADARKACADITLAEIVSGLEEVGRVOMTRRTLLGHAKIYYA 120	
QY 61 MHATDSKLIVASAOBQKLIWDTYTTNKVAHPLPSSNWTCAVAPSGNFVACGGIDNM 120	61 MHATDSKLIVASAOBQKLIWDTYTTNKVAHPLPSSNWTCAVAPSGNFVACGGIDNM 120	
Db 61 MHATDSKLIVASAOBQKLIWDTYTTNKVAHPLPSSNWTCAVAPSGNFVACGGIDNM 120	61 MHATDSKLIVASAOBQKLIWDTYTTNKVAHPLPSSNWTCAVAPSGNFVACGGIDNM 120	
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Db 121 CSIVSLKREGNVAKVSRELTAHGTGLSCRFDDNNVIYSSGDTTCALMIETGQOKYVF 180	121 CSIVSLKREGNVAKVSRELTAHGTGLSCRFDDNNVIYSSGDTTCALMIETGQOKYVF 180	
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Db 121 CSIVSLKREGNVAKVSRELTAHGTGLSCRFDDNNVIYSSGDTTCALMIETGQOKYVF 180	121 CSIVSLKREGNVAKVSRELTAHGTGLSCRFDDNNVIYSSGDTTCALMIETGQOKYVF 180	
QY 181 VGHGTGCKMSIAVSPDYKLTISGACDASAKIMDVRECTGQRTFTGHESDINAIICFFPGEA 240	181 VGHGTGCKMSIAVSPDYKLTISGACDASAKIMDVRECTGQRTFTGHESDINAIICFFPGEA 240	
Db 181 VGHGTGCKMSIAVSPDYKLTISGACDASAKIMDVRECTGQRTFTGHESDINAIICFFPGEA 240	181 VGHGTGCKMSIAVSPDYKLTISGACDASAKIMDVRECTGQRTFTGHESDINAIICFFPGEA 240	
QY 241 ICTGSDASCRFLPDLRADELLTAYSHESIIGITTVAFSLSGILLFAGYDGFNCNVMSD 300	241 ICTGSDASCRFLPDLRADELLTAYSHESIIGITTVAFSLSGILLFAGYDGFNCNVMSD 300	
Db 241 ICTGSDASCRFLPDLRADELLTAYSHESIIGITTVAFSLSGILLFAGYDGFNCNVMSD 300	241 ICTGSDASCRFLPDLRADELLTAYSHESIIGITTVAFSLSGILLFAGYDGFNCNVMSD 300	
QY 301 KCEVGVLSGHDNRVSCGLVTDGNAVATGSGMSDFLKIYNN 340	301 KCEVGVLSGHDNRVSCGLVTDGNAVATGSGMSDFLKIYNN 340	

Db 301 KSERVGLSGHNDNRVSCLGVTADGMAVATGSMDSFLKIN 340

RESULT 2

US-08-190-802A-38

Sequence 38, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0860

TELEFAX: (415) 324-0860

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: G-Beta 1 bovine, Fig. 21

US-08-190-802A-38

Query Match

Best Local Similarity 87.0%; Score 1573; DB 1; Length 340;

Matches 263; Conservative 31; Mismatches 26; Indels 0; Gaps 0;

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 1 MGEMLQKQEAOLKQJADARKACADITLAEIVSGLEVGVGRVOMTRRTLRGLAKIYA 60

Db 241 FTTGSDATCRFLDLRADQELMTYSHDNITCGITSVAFSRSGRLLAGYDFDNCNIMWDM 300
QY 301 KCEVGVLSGHDNRVSCGLVTADGMAVATGSDWDFLKTWN 340
Db 301 KEDRAGVLAGHDNRVSCGLVTDDGMAVATGSDWDFLKTWN 340

RESULT 4

US-09-147-826B-2

Sequence 2, Application US/09147826B

Patent No. 6251853

GENERAL INFORMATION:

APPLICANT: Siftart, Winfield

TITLE OF INVENTION: PTX-SENSITIVE G PROTEINS, THEIR PREPARATION AND USE

FILE REFERENCE: 1135-0003

CURRENT APPLICATION NUMBER: US/09/147,826B

PRIOR FILING DATE: 1997-08-29

PRIOR APPLICATION NUMBER: DE 196 37 518.5

PRIOR FILING DATE: 1996-09-13

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin version 3.0

SEQ ID NO: 2

LENGTH: 299

TYPE: PRT

ORGANISM: Homo sapiens

US-09-147-826B-2

Query Match 84.1%; Score 1520.5; DB 4; Length 299;
Best Local Similarity 85.0%; Pred. No. 3.2e-148;
Matches 289; Conservative 7; Mismatches 3; Indels 41; Gaps 1;

QY 1 MEMEOLKOEAEOLKQIADARKACADITLAEVSGLEVGVGVOMRTTRTLRGHLAKIYA 60
Db 1 MEMEOLKOEAEOLKQIADARKACADITLAEVSGLEVGVGVOMRTTRTLRGHLAKIYA 60
QY 61 MHMATSCKLLVASODGKLIWDTYTNKVAHAIPLRSSWMTCAVAPSGNFVACGGLNDM 120
Db 61 MHMATSCKLLVASODGKLIWDTYTNKVAHAIPLRSSWMTCAVAPSGNFVACGGLNDM 120
QY 121 CSYLSKREGVAVKVSRELSAHTGYLSCCRFLDNNIYTSDDTTCALMDIETGOQKTVF 180
Db 121 CSYLSKREGVAVKVSRELSAHTGYLSCCRFLDNNIYTSDDTTCALMDIETGOQKTVF 180
QY 181 VGHTEGDSLAIVSPDYKLFISGACDASAKLMDVREGTCRQFTTGHSIDINAICTFPNGEA 240
Db 181 VGHTEGDSLAIVSPDYKLFISGACDASAKLMDVREGTCRQFTTGHSIDINAICTFPNGEA 240
QY 241 ICTGSDASCRFLDLRADQELMTYSHDNITCGITSVAFSRSGRLLAGYDFDNCNIMWDM 300
Db 241 ICTGSDASCRFLDLRADQELMTYSHDNITCGITSVAFSRSGRLLAGYDFDNCNIMWDM 300
QY 301 KCEVGVLSGHDNRVSCGLVTADGMAVATGSDWDFLKTWN 340
Db 301 KCEVGVLSGHDNRVSCGLVTADGMAVATGSDWDFLKTWN 340
QY 260 KSERVGLISGHDNRVSCGLVTADGMAVATGSDWDFLKTWN 299
Db 260 KSERVGLISGHDNRVSCGLVTADGMAVATGSDWDFLKTWN 299

RESULT 5

US-08-190-802A-45

Sequence 45, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESSES:

ADDRESS: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabiao, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GTP binding protein (squid), Fig. 28

US-08-190-802A-45

Query Match 81.1%; Score 1467; DB 1; Length 341;
Best Local Similarity 79.9%; Pred. No. 1.2e-142;
Matches 270; Conservative 30; Mismatches 38; Indels 0; Gaps 0;

QY 3 EMEOLKOEAEOLKQIADARKACADITLAEVSGLEVGVGVOMRTTRTLRGHLAKIYAMH 62
Db 4 EMEOLKOEAEOLKQIADARKACADITLAEVSGLEVGVGVOMRTTRTLRGHLAKIYAMH 62
QY 63 WATDSKLLVASODGKLIWDTYTNKVAHAIPLRSSWMTCAVAPSGNFVACGGLNDMCS 122
Db 64 WATDSKLLVASODGKLIWDTYTNKVAHAIPLRSSWMTCAVAPSGNFVACGGLNDMCS 122
QY 123 IYSLSKREGVAVKVSRELSAHTGYLSCCRFLDNNIYTSDDTTCALMDIETGOQKTVF 182
Db 124 IYSLSKREGVAVKVSRELSAHTGYLSCCRFLDNNIYTSDDTTCALMDIETGOQKTVF 182
QY 183 HTGDSMSLAIVSPDYKLFISGACDASAKLMDVREGTCRQFTTGHSIDINAICTFPNGEA 242
Db 184 HTGDSMSLAIVSPDYKLFISGACDASAKLMDVREGTCRQFTTGHSIDINAICTFPNGEA 242
QY 243 TGSDDASCRFLDLRADQELMTYSHDNITCGITSVAFSRSGRLLAGYDFDNCNIMWDM 302
Db 244 TGSDDASCRFLDLRADQELMTYSHDNITCGITSVAFSRSGRLLAGYDFDNCNIMWDM 302
QY 303 ERVGVLSGHDNRVSCGLVTADGMAVATGSDWDFLKTWN 340
Db 304 ERVGVLSGHDNRVSCGLVTADGMAVATGSDWDFLKTWN 341

RESULT 6

US-08-190-802A-40

Sequence 40, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESSES:

ADDRESS: Dehlinger & Associates

STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 340 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: G- BETA DROSOPH, Fig. 23
 US-08-190-802A-40

Query Match 80.3%; Score 1452; DB 1; Length 340;
 Best Local Similarity 76.5%; Pred. No. 4.2e-141;
 Matches 260; Conservative 38; Mismatches 42; Indels 0; Gaps 0;

1 MGEEOLKQAEOLKKQIADARACADITLAEVSGLEVGRVOMRTTRTLRGHLAKIYA 60
 1 MNEIDSLRQESLKNATIRAKACDITSLQATSLTEPIGRLOMTRRLRHLAKIYA 60
 61 MHNATDSKLVSASQDGLIYMDITTYTNKVAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 61 MHNMDNRNLVSASQDGLIYMDISHTNKHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 121 CSYISLKSREGNVAKSELNHHGYLSGCCRFDDNNITVSSGDTTCALMDIETGQOKTVF 180
 121 CSYINLKTREGNVAKSELNHHGYLSGCCRFDDNNITVSSGDTTCALMDIETGLOVTSF 180
 181 VGHGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFFPNGEA 240
 181 LGHGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFFPNGEA 240
 241 ICGTSDASCRFLDLRADQELTAVSHESIIGITSVAFSLSGRLLFAGYDENCNWDSTL 300
 241 FATGSDATCRFLDLRADQELTAVSHESIIGITSVAFSLSGRLLFAGYDENCNWDSTL 300
 301 KCEKRVGLSGHNRVSCGLVTADGMVAATGSMDSFLKTN 340
 301 KAERSGILAGHNRVSCGLVTENGMVAATGSMDSFLKTN 340

RESULT 7
 US-08-190-802A-39
 ; Sequence 39, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron, Dorit
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 326 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: G-Beta- bovine (2), Fig. 22
 US-08-190-802A-39

Query Match 78.4%; Score 1419; DB 1; Length 326;
 Best Local Similarity 78.5%; Pred. No. 9.8e-138;
 Matches 260; Conservative 28; Mismatches 33; Indels 10; Gaps 2;

15 KKOIDARACADITLAEVSGLEVGRVOMRTTRTLRGHLAKIYAMHATDSKLVSAS 74
 1 KKOIDARACADITLAEVSGLEVGRVOMRTTRTLRGHLAKIYAMHATDSKLVSAS 74
 75 QDGLIYMDITTYTNKVAIPLRSSWMTCAVAPSGNFVACGGIDNMCSYISLSR 129
 61 QDGLIYMDITTYTNKVAIPLRSSWMTCAVAPSGNFVACGGIDNMCSYISLSR 129
 130 EGNVKSRELNHHGYLSGCCRFDDNNITVSSGDTTCALMDIETGQOKTVFVGHGTGDCMS 189
 121 VSRFLPHTGTGLSCRFDDNNITVSSGDTTCALMDIETGQOKTVFVGHGTGDCMS 175
 190 LAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFFPNGEA 249
 176 LSIAPDGRTFVSGACDASAKLMDVREGTCROTFTGHESDINAICFFPNGEA 235
 250 CRFLDLRADQELTAVSHESIIGITSVAFSLSGRLLFAGYDENCNWDSTLKCERVGLS 309
 236 CRFLDLRADQELTAVSHESIIGITSVAFSLSGRLLFAGYDENCNWDSTLKCERVGLS 295
 310 GHNRVSCGLVTADGMVAATGSMDSFLKTN 340
 296 GHNRVSCGLVTADGMVAATGSMDSFLKTN 326

RESULT 8
 US-09-032-372-1
 ; Sequence 1, Application US/09032372
 ; Patent No. 6008337
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.

```

1  APPLICANT: Guegliet, Karl J.
2  APPLICANT: Yue, Henry
3  APPLICANT: tal, preeti
4  TITLE OF INVENTION: CELL CYCLE RELATED PROT
5  NUMBER OF SEQUENCES: 13
6  CROSSREFERENCE ADDRESS:
7  ADDRESSEE: Incyte Pharmaceuticals, Inc.
8  STREET: 3174 Porter Drive
9  CITY: Palo Alto
10 STATE: CA
11 COUNTRY: USA
12 ZIP: 94304
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Diskette
16 COMPUTER: IBM Compatible
17 OPERATING SYSTEM: DOS
18 SOFTWARE: FASTSEQ for Windows Version 2.0
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/09/032.372
22
23 FILING DATE: Herewith
24 CLASSIFICATION:
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER:
28
29 FILING DATE:
30
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Billings, Lucy J
33 REGISTRATION NUMBER: 36,749
34 REFERENCE/DOCKET NUMBER: PF-0478 US
35
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: 650-855-0555
38 TELEFAX: 650-845-4166
39
40 TELEX:
41
42 INFORMATION FOR SEQ ID NO: 1:
43
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 395 amino acids
46 TYPE: amino acid
47 STRANDEDNESS: single
48 TOPOLOGY: linear
49 IMMEDIATE SOURCE:
50
51 LIBRARY: SYMORAB01
52 CLONE: 78191
53
54 US-09-032-372-1

```

Query Match	52.3%	Score 946.5;	DB 3;	Length 395;
Best Local Similarity	51.9%;	Pred. No. 4.7e-89;		
Matches 177;	Conservative 56;	Mismatches 103;	Indels 5;	Gaps 3

```

0Y 4 MEOLKOEBOELKQJADAKKACADITIAELVSGLEVGRVOMRIRIKRLROGLLAIIMWM 6
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 54 LASTSEAESEKLGKLEEBERRALHVEHLQVAREALGOEFMKRRRLKGGHKNVLCMDV 11.3
QY 64 ATDSKLIVASADGKLJYMDFTYTNKVAIPILRSWMTQVATPAGSNFVACGLDNMCISI 12.3
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 CKDKRRIYSSODGKVLYMDSFNTNKELAVMPCTWMAACIAPASGCAIACGLDNKCSV 17.3
QY 124 YSL - KSRBGNKYVARELSAHTGYLSCCRFLD - DNNIVTSSGDTICALMDIETGQKTVF 18.6
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 174 YLPETDKNNEMAAKKSAVMHTNYLSASCFPNSMDMOILITASGDPTCALMVESEGLLOSF 23.3
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 VCHTBD -- CMSIAVSPDYKCLFTSGACDASAKTLMVREBCTQGFETGHSIDNALCFPPNG 23.8
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 HGHGADVLCGLDAPSETGNTVYSGGCDKKAAMWDRSQCYQAEETHESDINSRYRTPSG 29.9
QY 239 FAICTGSDASACRLFELRADDELAVASHESITCGITTSYAFSLGRLLFAGYDDENCVMD 29.6
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 294 DAFAGSGDDATCFRLYDLRADEVALIYSKESLIIFGASVSDFLSRLRLFAGYNDTYINWD 35.5
QY 299 SLKCRVAVYLSGHNDRVASCIGTADGMAVAMWDSPLKIM 33.9
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 354 VIKGSRVSTILFCHENKRVSTLKRVSFDGTCIFCGSGMDHTLRW 39.4

```

RESULT 9
US-08-190-802A-61

? Sequence 61, Application US/08190802A
 ? Patent No. 5519003
 ?
 ? GENERAL INFORMATION:
 ?
 ? APPLICANT: Mochly-Rosen, Daria
 ? APPLICANT: Ron, Dotit
 ? TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ? TITLE OF INVENTION: Thereof
 ? NUMBER OF SEQUENCES: 265
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Delhinger & Associates
 ? STREET: P.O. Box 60850
 ? CITY: Palo Alto
 ? STATE: CA
 ? COUNTRY: USA
 ? ZIP: 94306-0850
 ?
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: PatentIn Release #1.0, Version #1.25
 ?
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/190.802A
 ? FILING DATE: 01-FEB-1994
 ? CLASSIFICATION: 530
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Fabian, Gary R.
 ? REGISTRATION NUMBER: 33,875
 ? REFERENCE/DOCKET NUMBER: 8600-0139
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (415) 324-0880
 ? TELEFAX: (415) 324-0960
 ? INFORMATION FOR SEQ ID NO: 61:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 423 amino acids -
 ? TYPE: amino acid
 ? TOPOLOGY: unknown
 ? MOLECULE TYPE: protein
 ? HYPOTHETICAL: NO
 ? ANTI-SENSE: NO
 ? ORIGINAL SOURCE:
 ? INDIVIDUAL ISOLATE: STE4 - YEAST, Fig. 44
 ?
 ? US-08-190-802A-61

Query Match	35.3%;	Score 639;	DB 1;	Length 423;
Best Local Similarity	36.3%;	Pred. No. 2.1e-57;		
Matches 139;	Conservative 74;	Mismatches 124;	Indels 46;	Gaps 6

```

QY 3 ENEHOKOEBELKKOIAVARAKACDITLAEVSLLEV--GRVOMRRRLRLSHKLAKYA 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 38 KIEARQESKQJLHAIINAKKHKIDQASJFQMANVTSILTKKILKKNYILKGGHNNKISD 97

QY 61 MHMARDSKILVASODGKLIYWDITTYTKKVAHPLRBSRWMTCAAPSGNFVACGLDNN 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 98 FMSRBSRKILIASODGFMLIWDASGKLONAIPLDOSQWLSLCAISSPTLVASAGLNN 157

QY 121 CSYLSLKSREGV--KVSRELSAHGYSLCCRFLLDNNIVTSSDDTYCALMDJETGOOKT 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 158 CILYIR--SKENNVAQNVASIFKGHCICYISDIEFDMNHILASGDMCALMDIEKARVR 216

QY 179 VFVGHGTGDCMSIAVSPDKL-----FISGACDASAKIMVREBCTQOTTEGHESDINA 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 217 EYSDHIGDVALALAEPEPLIENSSMTFASCGSDGYTIYIWDSRSPSAVOSFIYVSDJNAL 276

QY 233 CFPNGEAICTGSDASCLFELIARDQEL-----TAYSH 266
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 REFQDQMSIVASDQKAIIMYDULRSDCSIAFSLFGRYEERTPTPTYMAANMEYNTAOSP 336

QY 267 ESILC-----GITSVAFSLSGRLFLFAGDDPNCNWMVSLSCGERGYVLSCHDNVSC 317
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 337 QYLTKTSSTSYLDNOGVASLDFSPASRLMISCTYIDGCVWYVYLGLGYALKEGHSRGVYG 396

```

QY 318 LGVADGMAVATGSDSEFLKIMN 340
: : : : :
Db 397 VRSSPDGLAVCTGSDMTKIMNS 419

RESULT 10
US-08-190-802A-27
; Sequence 27, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Theoref
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: RACK1 Amino Acid Sequence, Fig. 1C
; US-08-190-802A-27

Query Match 16.4%; Score 297.5; DB 1; Length 317;
Best Local Similarity 30.8%; Pred. No. 1.7e-22;
Matches 80; Conservative 46; Mismatches 119; Indels 15; Gaps 6;
QY 48 RRLRGLHAKIYAMHMTADSKLVASODGKLIYWDYTTNKVHAIPLRSSWMTCAVAP 107
: : : : :
Db 56 QRALRGSHFVSDVIVSSDGFALSGSWDGLRLMDLTGTTTRRFVGHTRDVLVAFSS 115
: : : : :
QY 108 SGNFVACGGLDMNCISYLSKREGVNVKRSRELSAHTGILSCRF--DDNNIVTSSG-DT 164
: : : : :
Db 116 DNRQIVSSSRKTKIKIMNTL--GVCKITYODESHSEWVSCVRFSPNSNPITIVSGGMDK 172
: : : : :
QY 165 TCALMDIETGQOKTVFVGHGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQFTG 224
: : : : :
Db 173 LVKVMNLANKLKTNNHIGHTGYLNTVTVSPDGLSCASGKDGQAMLDNKGKHLTYLDG 232
: : : : :
QY 225 HESDINACEFPNGEALICTGSDASCRFLDRA-----DDELTAVSHESTICGITSVA 277
: : : : :
Db 233 GDI-INALCFSPNRYWLCAT--GPSIKIMDLGKTIYDELKQEVISTSSKAEPPOCTSLA 290
: : : : :
QY 278 FSLSGRLFLAGYDDFNQNV 297

Db 291 WSADGOTLFLAGYTDNLVRVW 310

RESULT 11
US-08-190-802A-41
; Sequence 41, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Theoref
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: G-BETA HUMAN, Fig. 24
; US-08-190-802A-41

Query Match 16.4%; Score 297.5; DB 1; Length 317;
Best Local Similarity 30.8%; Pred. No. 1.7e-22;
Matches 80; Conservative 46; Mismatches 119; Indels 15; Gaps 6;
QY 48 RRLRGLHAKIYAMHMTADSKLVASODGKLIYWDYTTNKVHAIPLRSSWMTCAVAP 107
: : : : :
Db 56 QRALRGSHFVSDVIVSSDGFALSGSWDGLRLMDLTGTTTRRFVGHTRDVLVAFSS 115
: : : : :
QY 108 SGNFVACGGLDMNCISYLSKREGVNVKRSRELSAHTGILSCRF--DDNNIVTSSG-DT 164
: : : : :
Db 116 DNRQIVSSSRKTKIKIMNTL--GVCKITYODESHSEWVSCVRFSPNSNPITIVSGGMDK 172
: : : : :
QY 165 TCALMDIETGQOKTVFVGHGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQFTG 224
: : : : :
Db 173 LVKVMNLANKLKTNNHIGHTGYLNTVTVSPDGLSCASGKDGQAMLDNKGKHLTYLDG 232
: : : : :
QY 225 HESDINACEFPNGEALICTGSDASCRFLDRA-----DDELTAVSHESTICGITSVA 277
: : : : :
Db 233 GDI-INALCFSPNRYWLCAT--GPSIKIMDLGKTIYDELKQEVISTSSKAEPPOCTSLA 290
: : : : :
QY 278 FSLSGRLFLAGYDDFNQNV 297
Db 291 WSADGOTLFLAGYTDNLVRVW 310


```

RESULT 13
US-08-190-802A-62
; Sequence 62, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 86000-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: TRANSCRIPTION FACTOR TTF, Fig. 45
US-08-190-802A-62

```

	Query Match	Similarity	16.3%	Score 295;	DB 1;	Length 704;
	Best Local	Similarity	27.8%	Pred. No. 9,8e-22;		
	Matches	88;	Conservative	51;	Mismatches 123;	Indels 44; Gaps 9;
QY	55	LAKIYAMHATSKLLVSSASQDGLIVMDYTTNTNKVHALPLSSWMWCA-VAPSGNFVA	113			
Db	345	LKIKALALRRAS-KRLALSKDQLPSAVF---YIV-----LMSHGGVCAELISDSTMLA	393			
QY	114	CGGLDNMCSLYL-----KSREGNYK-----VSRELASHTGYL	146			
Db	394	CGFGDSVYRIWLSLFPANVFTLKDADSLRELKESADINVRMLDDRSGETVRSMLHTGVY	453			
QY	147	SCCRFLDDNNIYTS-SCDTCALMLPIETGQOKTVVYGHGDCMSLAVSDYKLYFTSGACD	205			
Db	454	YRCAPAPENMLLLSCSEDSFTRLMSLFTWSCVVTTRGHYVPWIVRFRPHGYFPVSCSYD	513			
QY	206	ASAKLMDVREGTCROTPEFGHESHDINAICFPFGEALICGSDASCRLLDLRADQGLTAYS	265			
Db	514	KTARIMALDDSNQALRFVFGHLSDDVUCVQFPHFMSNYVAAGSSDRYRLMDNNMTGOSVRLMT	573			
QY	266	-HESIIGITSVAFSLSGRLLFAGYDDENCVMWDSLKCEERYGVLSGHNNRVSLCLVTAD	324			
Db	574	GHKG---SVSSLAIFACAGRYLASGSVDHNIILIMWLSNSLVTTLRLRHISTYTTITTFSDG	630			
QY	325	MAVATGSDSFLKIVN 340				
Db	631	TVLAAAGLDNNILITLMD 646				

RESULT 14

US-08-188-582-5
Sequence 5, Application US/08188582
Patent No. 5534410

GENERAL INFORMATION:

APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 704 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-582-5

Query Match

16.3%; Score 295; DB 1; Length 704;
Best local similarity 27.8%; Pred. No. 9.8e-22;

Matches 88; Conservative 51; Mismatches 133; Indels 44; Gaps 9;

QY 55 LAKIYAMHATDLSKLVASODGKLIWMPTTYTNKVAHPIRLSSWVMTCAYAPSGNFVA 113
DB 345 LKLIKALREAS-KRLALSKDQPSAVF---YTV-----LNSHOGVCAELSDSTMLA 393
QY 114 CGGLDNMCISYSL-----KSREGNVK-----VSRELSAHTGYL 146
DB 394 CGGDDSVRLWSLTPAKRLTKADSLRELDEKESADINVRMLDNRSGEYTRSLMHTGPV 453
QY 147 SCRRFLDNNIVTS-SGDTTCALMDIETGQOKTVFVGHGTGDCMSLAVSPDYKLFISGACD 205
DB 454 YKRAFAEMMULLSCSDSTIRLSLITWSCVYTYGHVYFPWDVFAFHGYTFVSCSYD 513
QY 206 ASAKIMVREGTCROTFTGHESDINAIICFPNGEALCTGSDASCRFLRADQELTAVS 265
DB 514 KTAIIMTDSNOLARVYVGLSDVDCQFHPNSNYATVATGSSDRTVRLDMNMTGOSVRLMT 573
QY 266 HESIIIGITSVAFSLGRLLFAGYDDFNQVWDSLAKERCYVGLSHDNRVSCGLVTADG 324

DB 574 GHKG---SVSSLAFSACGRYLAGSYVDHNIITWDLNSGLVTLTHRTSTVTTTFESRDG 630

QY 325 MAVATGSMDSFLAKIWN 340

DB 631 TVLAAAGLDNNLTLM 646

RESULT 15

US-08-646-715-5
Sequence 5, Application US/08646715
Patent No. 5637686

GENERAL INFORMATION:

APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 704 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-715-5

Query Match

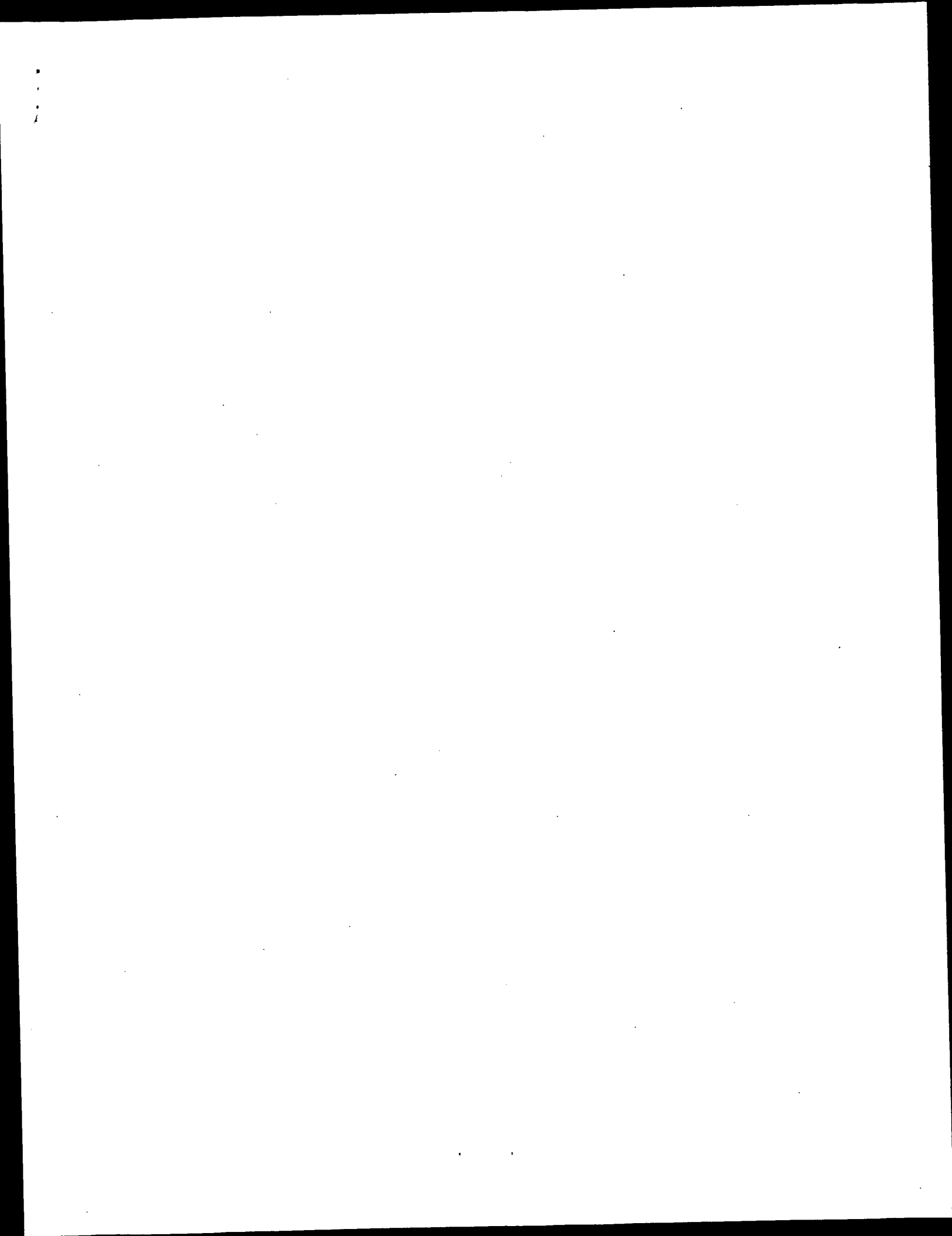
16.3%; Score 295; DB 1; Length 704;
Best local similarity 27.8%; Pred. No. 9.8e-22;

Matches 88; Conservative 51; Mismatches 133; Indels 44; Gaps 9;

QY 55 LAKIYAMHATDLSKLVASODGKLIWMPTTYTNKVAHPIRLSSWVMTCAYAPSGNFVA 113
DB 345 LKLIKALREAS-KRLALSKDQPSAVF---YTV-----LNSHOGVCAELSDSTMLA 393
QY 114 CGGLDNMCISYSL-----KSREGNVK-----VSRELSAHTGYL 146
DB 394 CGGDDSVRLWSLTPAKRLTKADSLRELDEKESADINVRMLDNRSGEYTRSLMHTGPV 453
QY 147 SCRRFLDNNIVTS-SGDTTCALMDIETGQOKTVFVGHGTGDCMSLAVSPDYKLFISGACD 205

Db 454 YCAFAPEMNLISCSEDESTIRLMSILTFWSCVVTYRGHYVPWVDFAPHGTYVSCSYD 513
 QY 206 ASAKLMDVREGTCROFETGHESDINAICEFPNGEAICTGSDDASCRLFDLRADOELTAYS 265
 Db 514 KTRRLMATSNOALRYFVGHLSVDVCOFHPNSNYVATGSSDRYRLMDNMTGOSVRLMT 573
 QY 266 -HESIICGITSVAESLSGRLLEFAGYDDFNCVWDSLKCEYGVLSGHDNRYSCLGYTADG 324
 Db 574 GHKG--SVSSIAFSACGRYLAAGSVDNHILIMDLNSGLVYTLRLRHSVYVTTTFESRDG 630
 QY 325 MAVATGSMDSFIKYN 340
 Db 631 TVLAAGLDNNLTLMW 646

Search completed: September 28, 2001, 10:28:39
 Job time: 30 sec



Fri Sep 28 10:45:09 2001

us-09-492-029-3.rsp

Page 1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 28, 2001, 10:29:45 : Search time 16.71 seconds
(without alignments)
697.000 Million cell updates/sec

Title: US-09-492-029-3
Perfect score: 1809
Sequence: 1 MGEKOLKQAEQLKQIAD.....TADGNVATGSMDSFLIKWN 340

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1809	100.0	340	1	GBB3_RAT
2	1794	99.2	340	1	GBB3_MOUSE
3	1771	97.9	340	1	GBB3_CANFA
4	1762	97.4	340	1	GBB3_HUMAN
5	1573	87.0	340	1	GBB1_HUMAN
6	1568	86.7	340	1	GBB1_XENLA
7	1532	84.2	340	1	GBB1_RAT
8	1516	83.8	340	1	GBB2_HUMAN
9	1515	83.7	340	1	GBB2_MOUSE
10	1495	82.6	340	1	GBB1_CAEBL
11	1493	82.5	340	1	GBB2_RAT
12	1482	81.9	340	1	GBB4_MOUSE
13	1477	81.6	340	1	GBB1_MOUSE
14	1467	81.1	340	1	GBB1_HUMAN
15	1457	80.3	340	1	GBB2_BOVIN
16	1452	80.3	340	1	GBB1_MOUSE
17	1425	67.7	340	1	GBB1_MOUSE
18	1425	67.7	340	1	GBB1_MOUSE
19	1189	52.3	340	1	GBB5_HUMAN
20	946.5	52.3	340	1	GBB5_MOUSE
21	945.5	52.3	340	1	GBB5_MOUSE
22	939.5	51.9	340	1	GBB5_MOUSE
23	844	46.7	340	1	GBB5_MOUSE
24	838	45.7	340	1	GBB5_MOUSE
25	827	45.7	340	1	GBB5_MOUSE
26	826	45.7	340	1	GBB5_MOUSE
27	825	45.6	340	1	GBB5_MOUSE
28	817	45.2	340	1	GBB5_MOUSE
29	817	45.2	340	1	GBB5_MOUSE
30	817	45.2	340	1	GBB5_MOUSE
31	792	43.6	340	1	GBB5_MOUSE
32	663	35.1	423	1	GBB_YEAST
33	635	35.1	423	1	GBB_YEAST

Result ID	Score	Query Match	Length	DB ID	Description
34	383.5	21.2	1356	1	HEP1_PODAN
35	341.5	18.9	742	1	PKWA_THECU
36	305.5	16.9	465	1	PRO4_YEAST
37	304.5	16.8	361	1	WDS_MOUSE
38	302	16.7	316	1	GBL1_MOUSE
39	300.5	16.6	317	1	GBL1_MOUSE
40	297.5	16.4	317	1	GBL1_MOUSE
41	295.5	16.3	317	1	GBL1_MOUSE
42	295	16.3	362	1	WDR5_HUMAN
43	295	16.3	704	1	T2D4_MOUSE
44	294	16.3	554	1	PRO4_MOUSE
45	293.5	16.2	318	1	GBL1_MOUSE

ALIGNMENTS

RESULT 1
ID GBB3_RAT
AC P52287; 1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3
DE (TRANSDUCIN BETA CHAIN 3).
GN GBB3.
OS Rattus norvegicus (Rat).
OC Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_Taxid=10116;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=SPRAGUE-DAWLEY; TISSUE=Heart;
RC MEDLINE=95047499; PubMed=7959013;
RA Ray K., Robshaw J.D.;
RT "Cloning and sequencing of a rat heart cDNA encoding a G-protein beta subunit related to the human retinal beta 3 subunit."
RL Gene 149:337-340(1994).
CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEIN (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GPROTEIN ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-SIGNALING INTERACTION.
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- TISSUE SPECIFICITY: EXPRESSED AT A HIGH LEVEL IN THE HEART AND AT A MUCH LOWER LEVEL IN THE BRAIN.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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CC -----
CC EMBL: L29090; AAA62620.1; -
CC HSSP: P04901; 1TBG.
CC InterPro: IPR001632; -
CC InterPro: IPR001680; 7.
CC Pfam: PF00400; WD40.
CC PRINTS: PR00319; GPROTEINB.
CC PRINTS: PR00320; GPROTEINB.
CC PROSITE: PS00678; WD_REPEATS_1; 3.
CC PROSITE: PS50082; WD_REPEATS_2; 5.
CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
CC Transducer: Repeat; WD repeat; Multigene family.
KW REPEAT
FT REPEAT 53
FT REPEAT 95
FT REPEAT 125
FT REPEAT 141
FT REPEAT 182
FT REPEAT 212
FT REPEAT 254
FT REPEAT 224

FT REPEAT 268 298 WD 6.
 REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37180 MW; 02041F754E81DA CRC64;

Query Match
 Best local similarity 100.0%; Score 1809; DB 1; Length 340;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEWOLKQEAEOBKQADITAEVSGLEVGRVQMTTRTGLHAKTYA 60
 DB 1 MGEWOLKQEAEOBKQADITAEVSGLEVGRVQMTTRTGLHAKTYA 60
 QY 61 MHWATDSKLLVASASODGKLIYMDYTTNKHVAIPLRSSWMTCAPSGNVACGGLDM 120
 DB 61 MHWATDSKLLVASASODGKLIYMDYTTNKHVAIPLRSSWMTCAPSGNVACGGLDM 120
 QY 121 CSYSLKREGNVKVSRELSTAGTGLSCRFDDNNITSSGDTTCALMDIETGQKTYF 180
 DB 121 CSYSLKREGNVKVSRELSTAGTGLSCRFDDNNITSSGDTTCALMDIETGQKTYF 180
 QY 181 VGHGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACFPNGEA 240
 DB 181 VGHGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACFPNGEA 240
 QY 241 ICGSDASCRFLDLRADOELTAYSHESIGITSVAFSLSGRLPAGYDDEFNCNWDLSL 300
 DB 241 ICGSDASCRFLDLRADOELTAYSHESIGITSVAFSLSGRLPAGYDDEFNCNWDLSL 300
 QY 301 KCEKRGVLSGHDNRVSCIGYADGMAVATGSDMSFLKTN 340
 DB 301 KCEKRGVLSGHDNRVSCIGYADGMAVATGSDMSFLKTN 340

RESULT 2

GBB3_MOUSE
 ID GBB3_MOUSE STANDARD: PRT: 340 AA.

AC 061011;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 30-MAY-2000 (rel. 39, Last sequence update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 3
 GN GNB3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
 RA Lu J., Gotrell J.H., Chinault A.C., Belmont J.W., Miller W.,
 RA Glubs R.A.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RP
 RC STRAIN=CF-1 / HARIAN; TISSUE=Retina;
 RX MEDLINE=97011591; PubMed=8858601;
 RT Williams C.J., Schultz R.M., Kopf G.S.;
 RT "G protein gene expression during mouse oocyte growth and maturation,
 RT Mol. Reprod. Dev. 44:315-323(1996)."
 RL
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC -1- SIMILARITY: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

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 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@1sb-sib.ch).
 CC EMBL: AC002397; AAC36013.1;
 DR EMBL: U38494; AAB01725.1;
 DR HSSP: P04901; IGP2.
 DR MGD: MGI:95785; Gnb3.
 DR InterPro: IPR001632;
 DR InterPro: IPR001680;
 DR Pfam: PF00400; WD40.2;
 DR PRINTS: PRO0319; GPROTEINB.
 DR PROSITE: PS00678; WD_REPEATS_1; 3;
 DR PROSITE: PS50082; WD_REPEATS_2; 5;
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37240 MW; 44BA0F8C0FEDEB1 CRC64;

Query Match
 Best local similarity 99.2%; Score 1794; DB 1; Length 340;
 Matches 336; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGEWOLKQEAEOBKQADITAEVSGLEVGRVQMTTRTGLHAKTYA 60
 DB 1 MGEWOLKQEAEOBKQADITAEVSGLEVGRVQMTTRTGLHAKTYA 60
 QY 61 MHWATDSKLLVASASODGKLIYMDYTTNKHVAIPLRSSWMTCAPSGNVACGGLDM 120
 DB 61 MHWATDSKLLVASASODGKLIYMDYTTNKHVAIPLRSSWMTCAPSGNVACGGLDM 120
 QY 121 CSYSLKREGNVKVSRELSTAGTGLSCRFDDNNITSSGDTTCALMDIETGQKTYF 180
 DB 121 CSYSLKREGNVKVSRELSTAGTGLSCRFDDNNITSSGDTTCALMDIETGQKTYF 180
 QY 181 VGHGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACFPNGEA 240
 DB 181 VGHGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACFPNGEA 240
 QY 241 ICGSDASCRFLDLRADOELTAYSHESIGITSVAFSLSGRLPAGYDDEFNCNWDLSL 300
 DB 241 ICGSDASCRFLDLRADOELTAYSHESIGITSVAFSLSGRLPAGYDDEFNCNWDLSL 300
 QY 301 KCEKRGVLSGHDNRVSCIGYADGMAVATGSDMSFLKTN 340
 DB 301 KCEKRGVLSGHDNRVSCIGYADGMAVATGSDMSFLKTN 340

RESULT 3

GBB3_CANFA
 ID GBB3_CANFA STANDARD: PRT: 340 AA.

AC P79147;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 3
 GN GNB3.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-ALASKAN MALAMUTE; TISSUE-Retina;
 RA MEDLINE-97409956; PubMed-9266671;
 RA Ahmedov N.B., Pirtiev N.I., Ray K., Acland G.M., Aguirre G.D.,
 RA Farber D.B.;
 RT "Structure and analysis of the transducin beta2-subunit gene, a
 RT candidate for inherited cone degeneration (cd) in the dog.";
 RL Gene 194:47-56(1997).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC
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 CC
 CC EMBL: U52916; AAC48760.1; -
 CC HSSP: P04901; 1TBG.
 CC InterPro: IPR001632; -
 CC InterPro: IPR001680; -
 CC Pfam: PF00400; WD40; 7.
 CC PRINTS: PR00319; GPROTEINB.
 CC PRINTS: PR00320; GPROTEINB.
 CC PROSITE: PS00678; WD_REPEATS_1; 3.
 CC PROSITE: PS50082; WD_REPEATS_2; 5.
 CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
 CC KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
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 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT REPEAT 340 340 WD 7.
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Query Match 97.9%; Score 1771; DB 1; Length 340;
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 Matches 331; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEMEQLKQEAQLKQIADARKACADITLAEVSGLEVGVGMQRTTRTLNGHLAKIYA 60
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 QY 61 MHMADSKILVASASODGKIYMDYTTNKNVHAIPRSSMVMCAAPSGNPAACGLDNN 120
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 QY 121 CSYILKSEGVNVKVSRELIAHTGYLSCCRFLDNNIYTSQDITCALMDIETGOQKTFV 180
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 QY 181 VGHTEGDCMSLAVSPDKFLISGACASAKLMDVREGTCRQFTGHESDINAICEFPEEA 240
 DB 181 VGHTEGDCMSLAVSPDKFLISGACASAKLMDVREGTCRQFTGHESDINAICEFPEEA 240
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 QY 301 KGERGVILSGHDNRVSCIGVADGMAVATGSGWDSFLKATWN 340
 DB 301 KGERGVILSGHDNRVSCIGVADGMAVATGSGWDSFLKATWN 340

RESULT 4
 ID GBB3_HUMAN STANDARD: PRT; 340 AA.
 AC P16520;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3
 DE (TRANSDUCIN BETA CHAIN 3).
 GN GNB3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90192801; PubMed-2107550;
 RA Levine M.A., Smallwood P.M., Moen P.T. Jr., Helman L.J., Ahn T.G.;
 RT "Molecular cloning of beta 3 subunit, a third form of the G protein
 RT beta-subunit polypeptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2329-2333(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96303695; PubMed-8723724;
 RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilly C.E.,
 RA Spanos S., Kallay T., Gibbs R.A.;
 RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
 RT genes at human chromosome 12p13.";
 RL Genome Res. 6:314-326(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Busch S., Dyhr W., Siffert W.;
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC
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 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA: 37221 MW: 896E706A1B0D74F CRC64:

Query Match 97.4%; Score 1762; DB 1; Length 340;
 Best local similarity 96.5%; Pred. No. 3,1e-147;
 Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGMELOKQAEQKQIDAKKACADITLAEVSGLEVGVQVQMTRETLGHLAKIYA 60
 DB 1 MGMELOKQAEQKQIDAKKACADITLAEVSGLEVGVQVQMTRETLGHLAKIYA 60
 QY 61 MHVATSKLLVSAQDGKILVMDYTTNRYVAIPLRSSWMTCAVPSGNFVACGGLDM 120
 DB 61 MHVATSKLLVSAQDGKILVMDYTTNRYVAIPLRSSWMTCAVPSGNFVACGGLDM 120
 QY 121 CSYLSKRSRGVNYKVSRELSAHTGYLSCRFDDNNITVSSGDTTCALMDIETGQKTVF 180
 DB 121 CSYLSKRSRGVNYKVSRELSAHTGYLSCRFDDNNITVSSGDTTCALMDIETGQKTVF 180
 QY 181 VGHGTGCMSLAVSPDYKFLFISGACDASAKIMDVRETCROTFTGHSDINATCFPNNGEA 240
 DB 181 VGHGTGCMSLAVSPDYKFLFISGACDASAKIMDVRETCROTFTGHSDINATCFPNNGEA 240
 QY 241 ICGSDASCRFLDRADELTAFTVSHESIICGITSVAFLSGLRFLAGYDDFNCAVWDSL 300
 DB 241 ICGSDASCRFLDRADELTAFTVSHESIICGITSVAFLSGLRFLAGYDDFNCAVWDSL 300
 QY 301 KCRVGVLSGHDNRVSCGLVTDGMAVATGSDWDFLKLNN 340
 DB 301 KCRVGVLSGHDNRVSCGLVTDGMAVATGSDWDFLKLNN 340
 RESULT 5
 ID GBL1_HUMAN STANDARD; PRT; 340 AA.
 AC P04901; P04697;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 1
 DE (TRANSDUCIN BETA CHAIN 1).
 GN GNB1.
 OS Homo sapiens (Human), Mus musculus (Mouse), Bos taurus (Bovine), and
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Caninata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606, 10090, 9913, 9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Human: TISSUE-Liver;
 RX MEDLINE-87030912; PubMed-3095147;
 RA Codina J., Stengel D., Woo S.L.C., Birnbaumer L.;
 RT "Beta-subunits of the human liver Gs/Gi signal-transducing proteins
 RT and those of bovine retinal rod cell transducin are identical.";
 RL FEBS Lett. 207:187-192(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Mouse; TISSUE-Adrenal gland;
 RA Qiu R., Schimke B.P.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Bovine;
 RX MEDLINE-86177563; PubMed-3083416;
 RA Fong H.K.W., Hurley J.B., Hopkins R.S., Mlake-Lye R., Johnson M.S.,
 RA Doolittle R.F., Simon M.I.;

RT "Repetitive segmental structure of the transducin beta subunit:
 RT homology with the CDC4 gene and identification of related mRNAs";
 RT proc. Natl. Acad. Sci. U.S.A. 83:2162-2166(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Bovine;
 RX MEDLINE-86030675; PubMed-2414128;
 RA Sugimoto K., Nukada T., Tanabe T., Takahashi H., Noda M., Minamino N.,
 RA Kangawa K., Matsuo H., Hirose T., Inayama S., Numa S.;
 RT "Primary structure of the beta-subunit of bovine transducin deduced
 RT from the cDNA sequence";
 RL FEBS Lett. 191:235-240(1985).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES-C. familiaris;
 RX MEDLINE-97445667; PubMed-9300552;
 RA Kyliana T., Pailin L., Hurwitz M.Y., Hurwitz R.L., Kommonen B.;
 RT "Cloning of the cDNA encoding rod photoreceptor
 RT cGMP-phosphodiesterase alpha and gamma subunits from the retinal
 RT degenerate Labrador retriever dog";
 RL Res. Vet. Sci. 62:293-296(1997).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF HETEROTRIMER.
 RX MEDLINE-96107343; PubMed-8521505;
 RA Wall M.A., Coleman D.E., Lee E., Iniguez-Lluhi J.A., Posner B.A.,
 RA Gilman A.G., Sprang S.R.;
 RT "The structure of the G protein heterotrimer G_i alpha 1 beta 1 gamma
 RT 2";
 RL Cell 83:1047-1058(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF BETA-GAMMA DIMER.
 RX MEDLINE-96149254; PubMed-8552196;
 RA Sondel J., Bohm A., Lambright D.G., Hamm H.E., Sigler P.B.;
 RT "Crystal structure of a G-protein beta gamma dimer at 2.1-A
 RT resolution";
 RL Nature 379:369-374(1996).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH PHOSDUCIN.
 RX MEDLINE-98416696; PubMed-9739091;
 RA Loew A., Ho Y.K., Blundell T., Bax B.;
 RT "Phosducin induces a structural change in transducin beta gamma";
 RL Structure 6:1007-1019(1998).
 CC -I- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -I- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -I- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL: X04526; CAA28207.1; -
 DR EMBL: U29055; AAC52905.1; -
 DR EMBL: X03073; CAA26875.1; -
 DR EMBL: M13236; AAA30792.1; -
 DR EMBL: M36430; AAA63265.1; -
 DR EMBL: Z75134; CAA99446.1; -
 DR PIR: A24853; RGHUB1.
 DR PIR: A24225; RGHOB1.
 DR PDB: 1GG2; 12-FEB-97.
 DR PDB: 1GP2; 12-FEB-97.
 DR PDB: 1TBG; 01-APR-97.
 DR PDB: 1AOR; 16-FEB-99.
 DR PDB: 1B9X; 23-FEB-99.
 DR PDB: 1B9Y; 23-FEB-99.
 DR MIM: 139380; -

DR MGD; MG1.95781; Gmb1.
 DR InterPro: IPR001632; -
 DR InterPro: IPR001680; -
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINB.
 DR PROSITE: PS00678; WD_REPEATS_1; 3.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 DR Transducer; Repeat; WD repeat; Multigene family; 3D-structure.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT CONFLICT 71 71 V -> L (IN REF. 4).
 SQ SOURCE 340 AA; 37377 MW; 896CB32D2686598 CRC64;

Query Match 87.0%; Score 1573; DB 1; Length 340;
 Best Local Similarity 83.2%; Pred. No. 1.2e-130;
 Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;

QY 1 MCEMOLKQAEOLKQIADAKACADITLAEIVSGLEVGVHVRMRTTGLHAKIYA 60
 DB 1 MSELDLQREAEOLKQIADAKACADITLAEIVSGLEVGVHVRMRTTGLHAKIYA 60
 QY 61 MHWATSKILVASASODGKLIYWDYTTNKVHAIPLRSSWMTCAVAPSGNVACGGLDNM 120
 DB 61 MHWGTSRLIVASASODGKLIYWDYTTNKVHAIPLRSSWMTCAVAPSGNVACGGLDNM 120
 QY 121 CSITSKSRGVKVSRELTAHTGYLSGCCRFDDNNIYSSGDTTCALMDIETGQOTTF 180
 DB 121 CSITNKTREGVKVSRELTAHTGYLSGCCRFDDNNIYSSGDTTCALMDIETGQOTTF 180
 QY 181 VGHGTGDMSLAVSPYKLFISGACDASAKIMDYREGTCRQFTGHESDINAICTFPNGEA 240
 DB 181 TGHGTGDMSLAVSPYKLFISGACDASAKIMDYREGTCRQFTGHESDINAICTFPNGEA 240
 QY 241 ICTGSDASCRFLPDLADQELTAHSHEIIIGITSVAFSLGRLIFGYDDFNCNWMDSL 300
 DB 241 FATGSDATCRFLPDLADQELTAHSHEIIIGITSVAFSLGRLIFGYDDFNCNWMDSL 300
 QY 301 KCERVGVLSGHDNRVSCIGVTADGMAVAATGSMDSFLKIWN 340
 DB 301 KADRAGVLAGHDNRVSCIGVTADGMAVAATGSMDSFLKIWN 340

RESULT 6
 GBB1_XENLA STANDARD; PRT; 340 AA.
 AC P79959;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 1
 DE (TRANSDUCIN BETA CHAIN 1) (XGBETA1).
 GN GNB1.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 CC NCB1_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97109512; PubMed=8951792;
 RA David E., Pequeveau L., Rizzoli K., Monier A., Knibbier B.,
 RA Audigier Y.;
 RT "The mRNA encoding a beta subunit of heterotrimeric GTP-binding
 RT proteins is localized to the animal pole of Xenopus laevis oocyte and
 RT embryos";

RL Mech. Dev. 59:141-151(1996).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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 CC -----
 DR EMBL: X86969; CAA60532.1; -
 DR HSSP: P04901; ITBG.
 DR InterPro: IPR001632; -
 DR InterPro: IPR001680; -
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINB.
 DR PROSITE: PS00678; WD_REPEATS_1; 3.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 DR Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37330 MW; DE036FE60A2D6A9 CRC64;

Query Match 86.7%; Score 1568; DB 1; Length 340;
 Best Local Similarity 82.9%; Pred. No. 3.2e-130;
 Matches 282; Conservative 30; Mismatches 28; Indels 0; Gaps 0;

QY 1 MCEMOLKQAEOLKQIADAKACADITLAEIVSGLEVGVHVRMRTTGLHAKIYA 60
 DB 1 MSELDLQREAEOLKQIADAKACADITLAEIVSGLEVGVHVRMRTTGLHAKIYA 60
 QY 61 MHWATSKILVASASODGKLIYWDYTTNKVHAIPLRSSWMTCAVAPSGNVACGGLDNM 120
 DB 61 MHWGTSRLIVASASODGKLIYWDYTTNKVHAIPLRSSWMTCAVAPSGNVACGGLDNM 120
 QY 121 CSITSKSRGVKVSRELTAHTGYLSGCCRFDDNNIYSSGDTTCALMDIETGQOTTF 180
 DB 121 CSITNKTREGVKVSRELTAHTGYLSGCCRFDDNNIYSSGDTTCALMDIETGQOTTF 180
 QY 181 VGHGTGDMSLAVSPYKLFISGACDASAKIMDYREGTCRQFTGHESDINAICTFPNGEA 240
 DB 181 TGHGTGDMSLAVSPYKLFISGACDASAKIMDYREGTCRQFTGHESDINAICTFPNGEA 240
 QY 241 ICTGSDASCRFLPDLADQELTAHSHEIIIGITSVAFSLGRLIFGYDDFNCNWMDSL 300
 DB 241 FATGSDATCRFLPDLADQELTAHSHEIIIGITSVAFSLGRLIFGYDDFNCNWMDSL 300
 QY 301 KCERVGVLSGHDNRVSCIGVTADGMAVAATGSMDSFLKIWN 340
 DB 301 KADRAGVLAGHDNRVSCIGVTADGMAVAATGSMDSFLKIWN 340

RESULT 7
 GBB1_RAT STANDARD; PRT; 340 AA.
 AC P54311;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

Transducer; Repeat; WD repeat; Multigene family.

KW REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT CONFLICT 195 195 D -> N (IN REF. 2).
 SQ SEQUENCE 340 AA; 37331 MW; 5D08FFA240ADEE6 CRC64;

Query Match 84.2%; Score 1523; DB 1; Length 340;
 Best Local Similarity 80.9%; Pred. No. 2.8e-126;
 Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

DB 1 MGEMOLKOEADQLKQIDARKACADITLAEVSGLEVGVOMRTTRTLRGLAKIYA 60
 1 MSELQLOEADQLKQIDARKACADITLAEVSGLEVGVOMRTTRTLRGLAKIYA 60
 DB 61 MHMTSKLIVASASQDGLIWDITTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 61 MHMTSKLIVASASQDGLIWDITTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 DB 121 CSYSLKREGNVRVRELSAHTGYISCCRFDDNNITVSSGDTTCALMDIETGQKTVF 180
 121 CSYSLKREGNVRVRELSAHTGYISCCRFDDNNITVSSGDTTCALMDIETGQKTVF 180
 DB 121 CSYSLKREGNVRVRELSAHTGYISCCRFDDNNITVSSGDTTCALMDIETGQKTVF 180
 121 CSYSLKREGNVRVRELSAHTGYISCCRFDDNNITVSSGDTTCALMDIETGQKTVF 180
 DB 181 VGHRTDMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFTGHESDINAIICFPNGEA 240
 181 VGHRTDMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFTGHESDINAIICFPNGEA 240
 DB 181 AGHSGDVMSLAPDGRFTVSGACDASIKIMDVREGTCROTFTGHESDINAIICFPNGEA 240
 181 AGHSGDVMSLAPDGRFTVSGACDASIKIMDVREGTCROTFTGHESDINAIICFPNGEA 240
 DB 241 ICTGSDASCRFLDLRAOELTAYSHESIICGITSVAFLSGLRLAGYDDFNCAVNDMSL 300
 241 ICTGSDASCRFLDLRAOELTAYSHESIICGITSVAFLSGLRLAGYDDFNCAVNDMSL 300
 DB 241 FTTGSDSTCRFLDLRAOELTAYSHESIICGITSVAFLSGLRLAGYDDFNCAVNDMSL 300
 241 FTTGSDSTCRFLDLRAOELTAYSHESIICGITSVAFLSGLRLAGYDDFNCAVNDMSL 300
 DB 301 KCERYVLSGHDNRVSCIGVTADGMAVATGSMDSFLKTNM 340
 301 KCERYVLSGHDNRVSCIGVTADGMAVATGSMDSFLKTNM 340
 DB 301 KGRAGVLAGHDNRVSCIGVTADGMAVATGSMDSFLKTNM 340
 301 KGRAGVLAGHDNRVSCIGVTADGMAVATGSMDSFLKTNM 340

RESULT 9
 GBB2_MOUSE STANDARD; PRT; 340 AA.
 ID GBB2_MOUSE
 AC P54312; (rel. 34. Created)
 DT 01-OCT-1996 (rel. 34. Last sequence update)
 DT 01-OCT-1996 (rel. 40. Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 2
 DE (TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT).
 GN GNB2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CELI;
 RC MEDLINE=97011591; PubMed=8858601;
 RA Williams C.J., Schultz R.M., Kopf G.S.;
 RT "G protein gene expression during mouse oocyte growth and maturation,
 RT and preimplantation embryo development.";
 RT Mol. Reprod. Dev. 44:315-323(1996).
 RL -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 RL INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 RL SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 RL GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 RL EFFECTOR INTERACTION.
 CC

CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN MEIOGONALLY INCOMPETENT OOCYTES.
 CC EXPRESSION INCREASES IN FULLY GROWN MEIOGONALLY INCOMPETENT OOCYTES.
 CC EXPRESSION THEN DECREASES DURING METAPHASE-II ARRESTED EGGS, ONE-
 CC CELL EMBRYO, TWO-CELL EMBRYO AND EIGHT-CELL EMBRYO STAGES, AND
 CC INCREASES AGAIN DURING BLASTOCYST STAGE.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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 CC
 CC EMBL; U34960; AAC7250.1; -
 CC EMBL; U38505; AAB01736.1; -
 CC HSP; P04901; 1TBG.
 CC MGD; MGI:95784; Gab2.
 CC InterPro; IPR001632; -
 CC InterPro; IPR001680; -
 CC Pfam; PF00400; WD40; 7.
 CC PRINTS; PR00319; GPROTEINB.
 CC PRINTS; PR00320; GPROTEINB.
 CC PROSITE; PS00678; WD_REPEATS_1; 3.
 CC PROSITE; PS00682; WD_REPEATS_2; 6.
 CC PROSITE; PS0294; WD_REPEATS_REGION; 1.
 CC Transducer; Repeat; Multigene family; polymorphism.
 KW REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT REPEAT 340 340 WD 7.
 FT VARIANT 248 248 S -> A (IN STRAIN CE1).
 FT SEQUENCE 340 AA; 37333 MW; F6C7DBAF9B43737D CRC64;

Query Match 83.8%; Score 1516; DB 1; Length 340;
 Best Local Similarity 80.3%; Pred. No. 1.2e-125;
 Matches 273; Conservative 32; Mismatches 35; Indels 0; Gaps 0;

DB 1 MGEMOLKOEADQLKQIDARKACADITLAEVSGLEVGVOMRTTRTLRGLAKIYA 60
 1 MSELQLOEADQLKQIDARKACADITLAEVSGLEVGVOMRTTRTLRGLAKIYA 60
 DB 61 MHMTSKLIVASASQDGLIWDITTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 61 MHMTSKLIVASASQDGLIWDITTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 DB 61 MHMTSKLIVASASQDGLIWDITTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 61 MHMTSKLIVASASQDGLIWDITTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 DB 181 VGHRTDMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFTGHESDINAIICFPNGEA 240
 181 VGHRTDMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFTGHESDINAIICFPNGEA 240
 DB 181 AGHSGDVMSLAPDGRFTVSGACDASIKIMDVREGTCROTFTGHESDINAIICFPNGEA 240
 181 AGHSGDVMSLAPDGRFTVSGACDASIKIMDVREGTCROTFTGHESDINAIICFPNGEA 240
 DB 241 ICTGSDASCRFLDLRAOELTAYSHESIICGITSVAFLSGLRLAGYDDFNCAVNDMSL 300
 241 ICTGSDASCRFLDLRAOELTAYSHESIICGITSVAFLSGLRLAGYDDFNCAVNDMSL 300
 DB 241 FTTGSDSTCRFLDLRAOELTAYSHESIICGITSVAFLSGLRLAGYDDFNCAVNDMSL 300
 241 FTTGSDSTCRFLDLRAOELTAYSHESIICGITSVAFLSGLRLAGYDDFNCAVNDMSL 300
 DB 301 KCERYVLSGHDNRVSCIGVTADGMAVATGSMDSFLKTNM 340
 301 KCERYVLSGHDNRVSCIGVTADGMAVATGSMDSFLKTNM 340
 DB 301 KGRAGVLAGHDNRVSCIGVTADGMAVATGSMDSFLKTNM 340
 301 KGRAGVLAGHDNRVSCIGVTADGMAVATGSMDSFLKTNM 340

RESULT 10
 GBB1_CAEL STANDARD; PRT; 340 AA.
 ID GBB1_CAEL
 AC P17343; Q19394;

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DT 01-AUG-1990 (Rel. 15, Created)
DR 15-JUL-1998 (Rel. 15, Last sequence update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1.
GN GPR-1 OR F13D12.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RX MEDLINE=90250769; PubMed=2110981;
RA van der Voorn L., Gebbink M., Plasterk R.H.A., Ploegh H.L.;
RT "characterization of a G-protein beta-subunit gene from the nematode
RT C. elegans";
RJ Mol. Biol. 213:17-26(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RA Coles L.;
RL Submitted (Apr-1995) to the EMBL/Genbank/DBJ databases.
CC -1 FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSDUCER
CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC GTPase ACTIVITY, FOR REPLACEMENT OF GTP BY GTP, AND FOR G PROTEIN-
CC EFFECTOR INTERACTION.
CC -1 SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1 SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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DR EMBL: X17497; CAA35532.1; -
DR EMBL: Z49127; CAA88948.1; -
DR PIR: S09591; RCKWB.
DR HSSP: P04901; ITBG.
DR WormRep: F13D12.7; CE02186.
DR InterPro: IPR001632; -
DR InterPro: IPR001680; -
DR Pfam: PF004400; WD40; 7.
DR PRINTS: PRO0319; GPROTEINB.
DR PROSITE: PRO0678; GPROTEINBPT.
DR PROSITE: PSS0082; WD_REPEATS_1; 3.
DR PROSITE: PSS0294; WD_REPEATS_REGION; 1.
KW Transducer; Repeat; WD repeat; Multigene family.
FT REPEAT 53 83 WD 1.
FT REPEAT 95 125 WD 2.
FT REPEAT 141 170 WD 3.
FT REPEAT 182 212 WD 4.
FT REPEAT 224 254 WD 5.
FT REPEAT 268 298 WD 6.
FT REPEAT 310 340 WD 7.
FT CONFLICT 240 240
FT SEQUENCE 340 AA; 37491 MW; 01FA08AD8D1A5ECF1 CRC64;

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[illegible]

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Db      6  MHMADSRNLVSAQSDKGLIWMDSYTTNKVAHPILRSSWMYTCAYAPSSGFVACGLDNI 120
Oy      121  CSIYLSARENNKVSRELSAHFGYLSCCRFLDDNNIVTSSGPTCALMDIETGOQKTFV 180
Db      121  CSIYLSKTRREGNVRVSRRLPGHGYLSCRRFLDDNQIVTSSGWTALMDIETGOQCTAF 180
Oy      181  VGHGDCMSLAVSPDKFLFISACASAKMLDVREGTCROTFTGHSBDINAIACFPNGEA 240
Db      181  TGHGDMVMSLSLSPDPRFTISACASAKMLDINDGCKOTFFGHESDINAVAFPPSNR 240
Oy      241  ICGSDSACSRFLFDLRADELTVASHEHSIIIGTIVSFSLSGILLFAGYDDENCWMDSL 300
Db      241  FATGSDATCRFLFDIRADDELTVAMYSHDNIIGTIVSAFKSGRLLFAGIDPFNCNWMDSM 300
Oy      301  KCRVGVLSGHNVRVSCGVADPADMAVATGSPMSFLKTN 340
Db      301  ROERAGVLAGHDNRVSCIGYTEDMAVCTGSMDSFLKTN 340

RESULT 11
GBB2_RAT
ID      GBB2_RAT      STANDARD;      PRT;      340 AA.
AC      P54313;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      01-OCT-2000 (Rel. 40, Last annotation update)
DE      GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 2
DE      (TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT).
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      NC1;taxid=10116;
RP      [1]
RC      SEQUENCE FROM N.A.
RL      STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RL      Kuroda S., Tokunaga C., Konishi H., Kikawa U.;
RA      Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS ARE
CC      INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
CC      SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC      GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC      EFFECTOR INTERACTION.
CC      -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC      -1- SIMILARITY: CONTAINS 7 WD REPEATS (TTP-ASP DOMAINS).
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as their content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U34959; AAC72248.1; -
DR      HSSP; P04901; ITRG
DR      InterPro; IPR001632; -
DR      InterPro; IPR001680; -
DR      Pfam; PF00400; WD40; 7.
DR      PRINTS; PR00319; GPROTEINB.
DR      PRINTS; PR00320; GPROTEINBRT.
DR      PROSITE; PS00678; WD_REPEATS_1; 3.
DR      PROSITE; PS50082; WD_REPEATS_2; 6.
DR      PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW      Transducer; Repeat; WD repeat; Multigene family.
FT      REPEAT 53 83 WD 1.
FT      REPEAT 95 125 WD 2.
FT      REPEAT 141 170 WD 3.
FT      REPEAT 182 212 WD 4.
FT      REPEAT 224 254 WD 5.
FT      REPEAT 268 298 WD 6.
FT      REPEAT 310 340 WD 7.
SQ      SEQUENCE 340 AA; 37500 MW; 1A60E275C5B71BB CXC64;

```


SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GTPASE ACTIVITY. FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.

-1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).

-1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

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CC

DR EMBL: Z23105; CAA80652.1; -

DR HSP: P04901; IGP2.

DR InterPro: IPR001632; -

DR InterPro: IPR001680; -

DR Pfam: PF00400; WD40; 7.

DR PRINTS: PR00319; GPROTEINB.

DR PRINTS: PR00320; GPROTEINBPT.

DR PROSITE: PS00678; WD_REPEATS_1; 2.

DR PROSITE: PS50082; WD_REPEATS_2; 5.

DR PROSITE: PS50294; WD_REPEATS_REGION; 1.

DR Transducer: Repeat; WD repeat.

FT REPEAT 54 84 WD 1.

FT REPEAT 96 126 WD 2.

FT REPEAT 142 171 WD 3.

FT REPEAT 183 213 WD 4.

FT REPEAT 225 255 WD 5.

FT REPEAT 269 299 WD 6.

FT REPEAT 311 341 WD 7.

SEQUENCE 341 AA; 37320 MW; 4A2662588307592E CRC64;

Query Match 81.9%; Score 1482; DB 1; Length 341;
Best Local Similarity 80.2%; Pred. No. 1,1e-122;
Matches 271; Conservative 29; Mismatches 38; Indels 0; Gaps 0;

QY 3 EMBL:K0EAEOLKQIADARRKACADITLAEVSGLEVGRVOMRTTRTLRGLAKIYA 62
DB 4 DLEALRTEQLKNOIRKARKAGDTTLAOCSGVEAGRIOMRTTRTLRGLAKIYA 63
QY 63 WATDSKLLVASODGKLIWDTYTNKVHAIPLRSSWMTCAYAPSGNFVACGGIDNCS 122
DB 64 WADSDSNLVASODGKLIWDTYTNKVHAIPLRSSWMTCAYAPSGNFVACGGIDNCS 123
QY 123 IYSLKSRGNVYKRELTAHTGYLSGCRFLDNNITVSSGDTTCALMDIETGQOKTVFV 182
DB 124 IYSLKTRGNVYKRELTAHTGYLSGCRFLDNNITVSSGDTTCALMDIETGQOKTVFV 183
QY 163 HTGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFTGHESDINAICFPNGEA 242
DB 184 HTGDMVSLSTSPDFTYFRTYGACDASAKIMDVREGTCROTFTGHESDINAICFPNGEA 243
QY 243 TGSDDASCRFLDRLADDELTAHSHESIIIGITSVAFFSLGRLLFAGYDDEFCNVMWDSLKC 302
DB 244 TGSDDATCRFLDRLADDELTAHSHESIIIGITSVAFFSLGRLLFAGYDDEFCNVMWDSLKC 303
QY 303 ERVGVLSGHDNRVYKLVATADGMAVATGSMDSFLKIWN 340
DB 304 ETHGVLAGHDNRVYKLVATADGMAVATGSMDSFLKIWN 341

RESULT 14
GB1 HOMAM
ID GB1 HOMAM STANDARD; PRT; 340 AA.
AC 045040;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TRANSDUCER BINDING PROTEIN G(1)/G(5)/G(7) BETA SUBUNIT 1
(TRANSDUCIN BETA CHAIN 1).

GN GETH1.
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_Taxid=6706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98410740; PubMed=9740024;
RA Xu F., Hollins B., Landers T.M., McClintock T.S.;
RT "Molecular cloning of a lobster Gbeta subunit and Gbeta expression in olfactory receptor neuron dendrites and brain neuropil."
RL J. Neurobiol. 36:525-536(1998).
CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -----
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CC EMBL: AF044735; AAC02998.1; -
DR InterPro: IPR001632; -
DR InterPro: IPR001680; -
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00319; GPROTEINB.
DR PRINTS: PR00320; GPROTEINBPT.
DR PROSITE: PS00678; WD_REPEATS_1; 3.
DR PROSITE: PS50082; WD_REPEATS_2; 6.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR Transducer: Repeat; WD repeat; Multigene family.
KW TRANSFER; Repeat; WD repeat; WD 1.
FT REPEAT 53 83 WD 1.
FT REPEAT 95 125 WD 2.
FT REPEAT 141 170 WD 3.
FT REPEAT 182 212 WD 4.
FT REPEAT 224 254 WD 5.
FT REPEAT 268 298 WD 6.
FT REPEAT 310 340 WD 7.
SEQUENCE 340 AA; 37409 MW; 3483245F9291D82E CRC64;

Query Match 81.6%; Score 1477; DB 1; Length 340;
Best Local Similarity 78.2%; Pred. No. 3e-122;
Matches 266; Conservative 35; Mismatches 39; Indels 0; Gaps 0;

QY 1 EMBL:K0EAEOLKQIADARRKACADITLAEVSGLEVGRVOMRTTRTLRGLAKIYA 60
DB 1 MNDLSLRQAEELKNTINDARKNALDITLVATAGMPDGRIGQRTTRTLRGLAKIYA 60
QY 61 MHWATDSKLLVASODGKLIWDTYTNKVHAIPLRSSWMTCAYAPSGNFVACGGIDN 120
DB 61 MHWGSDSNLVASODGKLIWDTYTNKVHAIPLRSSWMTCAYAPSGNFVACGGIDN 120
QY 121 CYSYSLKSRGNVYKRELTAHTGYLSGCRFLDNNITVSSGDTTCALMDIETGQOKTVF 180
DB 121 CYSYSLKTRGNVYKRELTAHTGYLSGCRFLDNNITVSSGDTTCALMDIETGQOKTVF 180
QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFTGHESDINAICFPNGEA 240
DB 181 TGHGDMVSLSTSPDFTYFRTYGACDASAKIMDVREGTCROTFTGHESDINAICFPNGEA 240
QY 241 ICGSDASCRFLDRLADDELTAHSHESIIIGITSVAFFSLGRLLFAGYDDEFCNVMWDSL 300
DB 241 FATGSDATCRFLDRLADDELTAHSHESIIIGITSVAFFSLGRLLFAGYDDEFCNVMWDSL 300

QY 301 KCEVGVLSGHDNRVSCIGVTADGMAVATGSDSFLKIMN 340
 DB 301 RTERAGVLAGHDNRVSCIGVTEDGMAVATGSDSFLKIMN 340

RESULT 15

GMB2_BOVIN STANDARD; PRT; 326 AA.

AC P11017;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 2
 (TRANSDUCER BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT) (FRAGMENT).
 GN GNB2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NX NCBI_TaxID=9913;
 [1]

SEQUENCE FROM N.A.
 RA MEDLINE=87231903; PubMed=3108879;
 RA Fong H.K.W., Amatruda T.T. III, Birren B.W., Simon M.I.;
 "Distinct forms of the beta subunit of GTP-binding regulatory
 RT proteins identified by molecular cloning.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3792-3796(1987).
 [2]

SEQUENCE OF 88-302 FROM N.A.
 RA MEDLINE=87317607; PubMed=3114742;
 RA Gao B., Gilman A.G., Robishaw J.D.;
 "A second form of the beta subunit of signal-transducing G proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6122-6125(1987).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

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 DR EMBL: M16480; AAA30553.1; -;
 DR EMBL: M36431; AAA62717.1; -;
 DR EMBL: M16539; AAA30552.1; -;
 DR PIR: A26617; RGNB02.
 DR HSSP: P04901; 1GP2.
 DR InterPro: IPR001680; -;
 DR Pfam: PF00400; WD40; 7;
 DR PROSITE: PS00678; WD_REPEATS_1; 3;
 DR PROSITE: PS50082; WD_REPEATS_2; 6;
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT NON_TER 1
 FT REPEAT 39 69 WD 1.
 FT REPEAT 81 111 WD 2.
 FT REPEAT 127 156 WD 3.
 FT REPEAT 168 198 WD 4.
 FT REPEAT 210 240 WD 5.
 FT REPEAT 254 284 WD 6.
 FT REPEAT 296 326 WD 7.
 FT CONFLICT 271 271 L -> V (IN REF. 2).
 SQ SEQUENCE 326 AA; 35645 MW; EEPB0EF5BCC5IB23 CRC64;

Query Match 81.1%; Score 1467; DB 1; Length 326;

Best local similarity 81.0%; Pred. No. 2.2e-121;
 Matches 264; Conservative 29; Mismatches 33; Indels 0; Gaps 0;
 QY 15 KQIADARRACADITLAEVSGLEEVGRVOMRTRRTLLGHLAKIYANMWMDSKLVSAS 74
 DB 1 RQIRDFARACDSDSTLTQTAGLDPVGRIQMRTTRTLGHLAKIYANMWMGDSRLVSAS 60
 QY 75 ODGKLIWDTYTNKVNVAIPLRSSWMTCAVAPSGNFVACGGLDNMCSIYSLKREGNVK 134
 DB 61 ODGKLIWDTYTNKVNVAIPLRSSWMTCAVAPSGNFVACGGLDNMCSIYSLKREGNVK 120
 QY 135 VSRELSTHTGYLSCCRFLDDNNIYVSSGDTTCALMDIETGQQTVPVGHGDCMSLAVSP 194
 DB 121 VSRELPGHTGYLSCCRFLDDNNIYVSSGDTTCALMDIETGQQTVPVGHGDCMSLAVSP 180
 QY 195 DYKLFISACACASAKLMDVREGTCRQTFPGHESDINAIICFPNGEAIICVSDPASCRLD 254
 DB 181 DGRFVSACDASIKLMDVREGTCRQTFPGHESDINAIICFPNGEAIICVSDPASCRLD 240
 QY 255 LRADQELTAVSHESIIGITSVAFSLSGRLFPAGYDPCNVMYDSIKCEVGVLSGHDNR 314
 DB 241 LRADQELTAVSHESIIGITSVAFSLSGRLFPAGYDPCNVMYDSIKCEVGVLSGHDNR 300
 QY 315 VSCIGVTRADGMAVATGSDSFLKIMN 340
 DB 301 VSCIGVTRADGMAVATGSDSFLKIMN 326

Search completed: September 28, 2001, 10:34:28
 Job time: 283 sec

Fri Sep 28 10:45:09 2001

us-09-492-029-3.rsp

On process: 1
Run on: September 28, 2001, 10:29:25 ; Search time 38.04 Seconds
(without alignments)
1182.537 Million cell updates/sec

Title: US-09-492-029-3
 Perfect score: 1009
 Sequence: 1 MGEMQLKQEAQLKQIAD.....TADGMAVATGSMDSFLKIWN 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:	425026 seqs, 132305027 residues	425026
Total number of hits satisfying chosen parameters:		

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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```

post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

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Database : SPTREMBL_16:*
1: sp archaea:*
```

```

1:  sp.archaea: *
2:  sp.bacteria: *
3:  sp.fungi: *
4:  sp.human: *
5:  sp.invertebrate: *
6:  sp.mammal: *
7:  sp.mhc: *
8:  sp.organelle: *
9:  sp.phage: *
10: sp.plant: *
11: sp.podent: *
12: sp.unclassified: *
13: sp.vertebrate: *
14: sp.virus: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description
No						
1	167.0	92.3	340	13	09DF69	09df69 ambystoma t
2	157.0	86.8	340	13	09DFH0	09dfh0 rattus norve
3	155.8	86.1	340	11	09QMG8	09qmg8 rattus norve
4	150.6	83.3	340	4	09HAV0	09hav0 homo sapien
5	149.6	82.7	340	11	09JHX8	09jhx8 mus musculu
6	123.5	69.3	352	3	09I887	09i887 cyriococcu
7	122.5	67.7	347	3	09HFS3	09hfs3 pneumocysti
8	121.5	67.2	352	3	074214	074214 emericella
9	95.7	52.9	358	3	09WJ31	09wj31 dirosophila
10	94.6	52.3	355	4	09HAN9	09han9 homo sapien
11	83.0	45.9	346	5	09WZ71	09wz71 calliphora
12	82.6	45.7	377	10	09XFK0	09xfk0 pisum sativi
13	82.5	45.5	377	10	09SM94	09sm94 pisum sativi
14	82.3	45.5	346	5	09WZ29	09wz29 dirosophila
15	81.1	44.8	377	10	09FV61	09fv61 nicotiana
16	79.4	43.9	380	10	064944	064944 aenea fatiu
17	73.9	40.9	426	3	09UTF3	09utf3 homo sapien
18	69.8	38.5	436	3	09Y7B8	09y7b8 kluyveriomyC
19	6.9	38.1	186	5	045041	045041 homarus ame

20	637	35.2	371	5	Q9XZV6	Q9XZV6 gredia cydo
21	601	33.2	123	11	Q61621	Q61621 mus musculus
22	592.5	32.8	240	10	Q04056	Q04056 nicotiana t
23	313	17.3	1241	2	Q9XBD8	Q9XBD8 amycolatols
24	312	17.2	53425	4	Q43445	Q43445 homo sapien
25	310	17.1	1049	2	Q9ZEM4	Q9ZEM4 streptomyc
26	310	17.1	1676	2	Q9KX99	Q9KX99 streptomyc
27	309	17.1	579	5	Q76734	Q76734 dicystosteli
28	308.5	17.1	485	4	Q9NXY2	Q9NXY2 homo sapien
29	308	17.0	333	10	Q9SYU0	Q9SYU0 arabidopsis
30	308	17.0	520	4	Q43864	Q43864 homo sapien
31	305	16.9	502	5	Q74855	Q74855 schizosacch
32	305	16.9	521	4	Q43172	Q43172 homo sapien
33	299	16.5	473	10	Q9FLX9	Q9FLX9 arabidopsis
34	295.5	16.3	561	3	Q14432	Q14432 schizosacch
35	295.5	16.3	586	3	Q9UWG8	Q9UWG8 schizosacch
36	295	16.3	334	4	Q9NWX7	Q9NWX7 homo sapien
37	291.5	16.1	476	13	Q9J331	Q9J331 xenopus lae
38	288.5	15.9	318	5	Q96653	Q96653 trypanosoma
39	286.5	15.8	317	13	Q9W711	Q9W711 xenopus lae
40	285.5	15.8	481	5	Q9VPR4	Q9VPR4 drosophila
41	284	15.7	553	5	Q9VW10	Q9VW10 drosophila
42	284	15.7	587	5	Q44083	Q44083 caenorhabdi
43	283.5	15.6	391	5	Q9VU65	Q9VU65 drosophila
44	283.5	15.6	613	10	Q9EN19	Q9EN19 arabidopsis
45	281.5	15.6	480	5	Q96995	Q96995 drosophila

ALIGNMENTS

	RESULT	1	
Q9DFG9	PRELIMINARY:	PRT;	340 AA.
AC	G9DFG9		
DT	01-MAR-2001 (TREMBLrel. 16,	Created)	
DT	01-MAR-2001 (TREMBLrel. 16,	Last sequence update)	
DT	01-MAR-2001 (TREMBLrel. 16,	Last annotation update)	
DE	G-PROTEIN B3 SUBUNIT.		
OS	Ambystoma tigrinum (tiger salamander).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;		
OC	Ambystoma.		
OX	NCBI_TaxID=8305;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=RETINA;		
RA	Ryan J.C., Crouch R.K., Ma J.;		
RI	"Cloning and Characterization of G-protein Beta subunits from the		
RL	Salamander Retina.";		
SD	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.		
	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.		
	EMBL: AF277162; AAC1061.1; -		
	DRBML: AF277162; AAC1061.1; -		
	SEQUENCE 340 AA; 3725 MW; 6C284C110055ZDBE CXC64;		

Score 1670; DB 13; Length 340;

Query Match	92.56	Score	25	
Best Local Similarity	88.88	Pred. No.	3,1e-145	
Matches	302	Mismatches	13	Indels
		Conservative	25	Gaps

[illegible]

Db 181 MGTGDCMSLAVSPDFRIFVSGACDATAKMDIREGTCROTFTGHESDINAICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELTAYSHESITIGITSVAFLSGLRLPAGYDDFNCNWDLSL 300
 Db 241 VCTGSDATACRLFDLRADQELTAYSHESITIGITSVAFLSGLRLPAGYDDFNCNWDLSL 300
 QY 301 KCEKRGVLSGHDNRVSCIGVTADGMAVAATGWSDFLKTWN 340
 Db 301 KCEKRGVLSGHDNRVSCIGVTADGMAVAATGWSDFLKTWN 340

RESULT 2

Q9DFH0 PRELIMINARY: PRT: 340 AA.
 AC Q9DFH0: 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE G-PROTEIN BI SUBUNIT.
 OS Ambystoma tigrinum (Tiger salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;
 OX NCBI_TaxID=8305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ryan J.C., Crouch R.K., Ma J.;
 RT Cloning and Characterization of G-protein Beta subunits from the
 RL Salamander Retina.
 DR EMBL, AF277161; AAC31060.1; to the EMBL/GenBank/DBJ databases.
 SQ SEQUENCE 340 AA; 37332 MW; 84E1451FDD83D8F3 CMC64;

Query Match

Best Local Similarity 86.8%; Score 1570; DB 13; Length 340;
 Matches 282; Conservative 30; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGEHOLKOEAEOLKQIDARACADITLAEVLSGLVGRVGMRTRRRLRGLAKTYA 60
 Db 1 MSELQOLROEAEOLKQIDARACADITLAEVLSGLVGRVGMRTRRRLRGLAKTYA 60
 QY 61 MHAATDSKLLVSAOQKLIWDTYTNKVAIPLRSSWWTCAVAPSGNFVACGLDNN 120
 Db 61 MHAATDSKLLVSAOQKLIWDTYTNKVAIPLRSSWWTCAVAPSGNFVACGLDNN 120
 QY 121 CSTYLSKREGVAVKYSRELTAHTGTLSCRFLLDNNITVSSGDTTCALMDIETGQOTT 180
 Db 121 CSTYLSKREGVAVKYSRELTAHTGTLSCRFLLDNNITVSSGDTTCALMDIETGQOTT 180
 QY 181 VGHGTGMSLAVSPYKLFISGACDASAKIMDVREGTCROTFTGHESDINAICFPNGEA 240
 Db 181 VGHGTGMSLAVSPYKLFISGACDASAKIMDVREGTCROTFTGHESDINAICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELTAYSHESITIGITSVAFLSGLRLPAGYDDFNCNWDLSL 300
 Db 241 FATGSDATACRLFDLRADQELTAYSHESITIGITSVAFLSGLRLPAGYDDFNCNWDLSL 300
 QY 301 KCEKRGVLSGHDNRVSCIGVTADGMAVAATGWSDFLKTWN 340
 Db 301 KADRAGYLAGHDNRVSCIGVTADGMAVAATGWSDFLKTWN 340

RESULT 3

Q9QW8 PRELIMINARY: PRT: 340 AA.
 AC Q9QW8: 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DE G-PROTEIN BETA SUBUNIT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Puhl H.L., Iikeda S.R., Aronstam R.S.;
 RT Cloning and Characterization of Human G-protein Beta 4.
 DR EMBL, AF300648; AAC18442.1; to the EMBL/GenBank/DBJ databases.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Wang X.B., Funada M., Imai Y., Revey R.S., Ujike H., Vandenbergh D.J.,
 RT Uhl G.R.;
 RT cocaine sensitization.
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL, U88324; AAD00650.1; -.
 DR HSP, P04901; ITBG.
 DR Interpro: IPRO01632; -.
 DR Interpro: IPRO01680; -.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINBPT.
 DR PROSITE: PS00678; WD_REPEATS; UNKNOWN_3.
 DR SMART: SM00320; WD40; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 340 AA; 37387 MW; D9EBECB0FE7EC57 CMC64;

Query Match

Best Local Similarity 86.1%; Score 1558; DB 11; Length 340;
 Matches 280; Conservative 30; Mismatches 30; Indels 0; Gaps 0;

QY 1 MGEHOLKOEAEOLKQIDARACADITLAEVLSGLVGRVGMRTRRRLRGLAKTYA 60
 Db 1 MSELQOLROEAEOLKQIDARACADITLAEVLSGLVGRVGMRTRRRLRGLAKTYA 60
 QY 61 MHAATDSKLLVSAOQKLIWDTYTNKVAIPLRSSWWTCAVAPSGNFVACGLDNN 120
 Db 61 MHAATDSKLLVSAOQKLIWDTYTNKVAIPLRSSWWTCAVAPSGNFVACGLDNN 120
 QY 121 CSTYLSKREGVAVKYSRELTAHTGTLSCRFLLDNNITVSSGDTTCALMDIETGQOTT 180
 Db 121 CSTYLSKREGVAVKYSRELTAHTGTLSCRFLLDNNITVSSGDTTCALMDIETGQOTT 180
 QY 181 VGHGTGMSLAVSPYKLFISGACDASAKIMDVREGTCROTFTGHESDINAICFPNGEA 240
 Db 181 TGHTGVMSLAPDTRLFVSGACDASAKIMDVREGTCROTFTGHESDINAICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELTAYSHESITIGITSVAFLSGLRLPAGYDDFNCNWDLSL 300
 Db 241 FATGSDATACRLFDLRADQELTAYSHESITIGITSVAFLSGLRLPAGYDDFNCNWDLSL 300
 QY 301 KCEKRGVLSGHDNRVSCIGVTADGMAVAATGWSDFLKTWN 340
 Db 301 NADRAGYLAGHDNRVSCIGVTADGMAVAATGWSDFLKTWN 340

RESULT 4

Q9HAVO PRELIMINARY: PRT: 340 AA.
 AC Q9HAVO: 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT 4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Puhl H.L., Iikeda S.R., Aronstam R.S.;
 RT Cloning and Characterization of Human G-protein Beta 4.
 DR EMBL, AF300648; AAC18442.1; to the EMBL/GenBank/DBJ databases.

SEQUENCE 340 AA; 37567 MW; EDF085155AIEDC89 CRC64;

Query Match 83.3%; Score 1506; DB 4; Length 340;

Best Local Similarity 79.7%; Pred. No. 3.5e-130;

Matches 271; Conservative 35; Mismatches 34; Indels 0; Gaps 0;

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QY 1 MGEMLQKQAEQOLKQADARAKACADITTLAEVSGLEVGVQVQRTTTLRGLAKIYA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1 MSELQDLQAEQOLKQADARAKACNDATLVQITSNMDSVGRIGQRTTTLRGLAKIYA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 MHWAQSKLLVASASODGKLIWDTYTTNKVHAIPLRSSWMVTCAYAPSGNFVACGLDNN 120
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 61 MHMGYDSRLVASASODGKLIWDSYTNKMHAIPLRSSWMVTCAYAPSGNFVACGLDNI 120
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 121 CSYLSKREGVNVKVSRELSAHTGTLSCRFDDNNIYTSDDITCALMDIETGQOKTVF 180
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 121 CSYLNKTRGEGNVKVSRELPGHTGLSCRFDDSQIYVTSDDITCALMDIETGQOKTVF 180
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 181 VGHTEGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFFGHESDINACFPNGEA 240
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 181 TGHSDGVMSLSLSPDMRTFVSACDASSKIMDIRGKCRQSTGHVSDINAVSFPNGYA 240
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 241 ICTGSDDASCRFLDLRADQELTAYSHESITIGITSVAFLSGRLLPAGYDDFNCNMWDSL 300
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 241 FATGSDDAATCRFLDLRADQELLYSHDNICIGITSVAFLSGRLLPAGYDDFNCNMWDTL 300
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 301 KCEYGVLSGHDNRVSCIGVTADGMAVATGSDSFLKTN 340
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 301 KGDRAVGLAGHDNRVSCIGVTDGMAVATGSDSFLKTN 340
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 5
09JHX8 PRELIMINARY; PRT; 340 AA.

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AC 09JHX8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE G-PROTEIN BETA-4 SUBUNIT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Arnott M.I., Stoltz S.C., Jarvis S.E., Zamponi G.W.;
RT "Differential modulation of N-type alpha 1b and P/Q-type alpha 1A
   calcium channels by different G protein beta subunit isoforms.";
RL J. Physiol. 0:0-0(2000).
DR EMBL; AF277893; AAF82124.1; -.
DR InterPro; IPR001632; -.
DR InterPro; IPR001680; -.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00319; GPROTEINB.
DR PRINTS; PR00320; GPROTEINBPT.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.
KM Repeat; WD repeat.
SQ SEQUENCE 340 AA; 37379 MW; F06827EBC2F0E966 CRC64;

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Query Match 82.7%; Score 1496; DB 11; Length 340;
Best Local Similarity 79.4%; Pred. No. 2.9e-129;
Matches 270; Conservative 35; Mismatches 35; Indels 0; Gaps 0;

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QY 1 MGEMLQKQAEQOLKQADARAKACADITTLAEVSGLEVGVQVQRTTTLRGLAKIYA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1 MSELQDLQAEQOLKQADARAKACNDATLVQITSNMDSVGRIGQRTTTLRGLAKIYA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 MHWAQSKLLVASASODGKLIWDTYTTNKVHAIPLRSSWMVTCAYAPSGNFVACGLDNN 120
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 61 MHMGYDSRLVASASODGKLIWDSYTNKMHAIPLRSSWMVTCAYAPSGNFVACGLDNI 120
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 241 ICTGSDDASCRFLDLRADQELTAYSHESITIGITSVAFLSGRLLPAGYDDFNCNMWDSL 300
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 241 FATGSDDAATCRFLDLRADQELLYSHDNICIGITSVAFLSGRLLPAGYDDFNCNMWDTL 300
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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QY 121 CSYLSKREGVNVKVSRELSAHTGTLSCRFDDNNIYTSDDITCALMDIETGQOKTVF 180
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 121 CSYLNKTRGEGNVKVSRELPGHTGLSCRFDDSQIYVTSDDITCALMDIETGQOKTVF 180
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 181 VGHTEGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFFGHESDINACFPNGEA 240
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 181 TGHSDGVMSLSLSPDMRTFVSACDASSKIMDIRGKCRQSTGHVSDINAVSFPNGYA 240
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 241 ICTGSDDASCRFLDLRADQELTAYSHESITIGITSVAFLSGRLLPAGYDDFNCNMWDSL 300
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 241 FATGSDDAATCRFLDLRADQELLYSHDNICIGITSVAFLSGRLLPAGYDDFNCNMWDTL 300
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 301 KCEYGVLSGHDNRVSCIGVTADGMAVATGSDSFLKTN 340
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 301 KGDRAVGLAGHDNRVSCIGVTDGMAVATGSDSFLKTN 340
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 6

093887 PRELIMINARY; PRT; 352 AA.

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AC 093887;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE G-PROTEIN BETA SUBUNIT GPB1.
GN GPB1.
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H99;
RA Wang P., Perfect J.R., Heitman J.;
RT "The G-protein beta subunit GPB1 is required for mating in
   Cryptococcus neoformans and functions in a pathway distinct from the
   alpha subunit GPB1.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091120; AAD03596.1; -.
DR HSSP; P04901; ITBG.
DR InterPro; IPR001632; -.
DR InterPro; IPR001680; -.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00319; GPROTEINB.
DR PRINTS; PR00320; GPROTEINBPT.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.
DR SMART; SM00320; WD40; 1.
KM Repeat; WD repeat.
SQ SEQUENCE 352 AA; 37904 MW; 36CF4F16AA2C6AB5 CRC64;

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Query Match 69.3%; Score 1253; DB 3; Length 352;
Best Local Similarity 65.7%; Pred. No. 6.1e-107;
Matches 224; Conservative 56; Mismatches 53; Indels 8; Gaps 1;

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QY 8 KQEAQOLKQADARAKACADITTLAEVSGLEVGVQVQRTTTLRGLAKIYAMHWAQTS 67
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 12 RREADGKDKRRAARDQADTSLRAMATDPPPRITLKRRLKGLAKIYALHMAADT 71
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 68 KLVASASODGKLIWDTYTTNKVHAIPLRSSWMVTCAYAPSGNFVACGLDNNCSYLSK 127
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 72 KHIYASASODGKLIWDMATYTTNKVHAIPLRSSWMVTCAYAPSGNLVACGLDNCYSYLSR 131
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 128 -----SREGNVKVSRELSAHTGTLSCRFDDNNIYTSDDITCALMDIETGQOKTVF 179
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 132 GAGGAGGAGGAGGVKVARRELSAHSGYLSCCRFINDRQIYVSSGDMTCMLMDIEQGTITME 191
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 180 FVGHTEGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFFGHESDINACFPNGEA 239
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 192 FNDHTGVNVCISLAPNVLVSGACDATTAKVMDIRGKAVQITFGHSDINAAQFPNPD 251
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 240 AICTGSDASCRFLDLRADQELTAYSHESITIGITSVAFLSGRLLPAGYDDFNCNMWDS 299
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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DB 252 AFAIGSDASCKLFDLADRELINAYHNDNLICGTTAFISGAVLFDYDDINCNWMT 311
 QY 300 LKCEKRVGLSGHNRVSCGLVADGMAVATGSDMSFLKLN 340
 DB 312 LKGERIGVLGHNENRVSVMGSDGVALCTGSDMSLTKVMS 352

RESULT 7
 QHFS3 PRELIMINARY; PRT; 347 AA.

AC 09HFS3
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE GRANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.
 OS Pneumocystis carinii.
 OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
 OC Pneumocystis.
 OX NCBI_Taxid=4754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Puri V., Park J.G., Limper A.H., Thomas C.F. Jr.;
 RT "The Pneumocystis carinii guanine nucleotide-binding protein beta
 subunit."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF056565; AAC27720.1; -; FEE1495006E24882 CRC64;
 SQ SEQUENCE 347 AA; 38438 MW; FEE1495006E24882 CRC64;

Query Match 67.7%; Score 1225.5; DB 3; Length 347;
 Best Local Similarity 66.9%; Pred. No. 2e-104;
 Matches 222; Conservative 44; Mismatches 65; Indels 1; Gaps 1;

QY 9 QEADQLKQIADARKACADITLAEVSGLEVGVGMRTTRTLGHLAKIYAMHWATDSK 68
 DB 15 KEAYLEKIKKKKDELADTLRSMAGTLPIERLSIRVYTLKGHLAKIYAMHWSTDK 74
 QY 69 LLYASODGKLIWDTYTNKVHAIPLRSSVMWTCAYAPSGNPFACGGLDMCSYLSKS 128
 DB 75 HLVSASODGKLIWDTYTNKVHAIPLRSSVMWTCAYAPSGNPFACGGLDMCSYLSKS 134
 QY 129 REGNVKVSRELTAHTGYLSCCRFLDNNIYVSGDTTCALMDETGOOKTVEVHTGDCM 188
 DB 135 KDHAKIARELMAHTGYLSCCRFLSDQILITSSGDMCCLIMDTGSKIDFELHLDVM 194
 QY 189 SLAVSP-DYKLFISGACDASAKIMDVREGTCROTFTGHESDINACFPNGEALCTGSD 247
 DB 195 SLISHPTNPMLFVSGADDAFAKIMDIRIGSVQTFAGHESDINAVOYFPGNNAFATGSD 254
 QY 248 ASCLFELRADDELTAYSHEIIGITSVAFLSGRLFLAGYDFNCNVWDSLKCEKRVG 307
 DB 255 ASCLFELRADRELINOTSAANIMCGITISIFSNSGRLLFAGYDDFNKVMWDLGNRVGI 314
 QY 308 LSGHNRVSCGLVADGMAVATGSDMSFLKLN 339
 DB 315 LQGHNRVSCVGSVSGDRLATGSDMSLTKIM 346

RESULT 8
 074214 PRELIMINARY; PRT; 352 AA.

AC 074214
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE G-PROTEIN BETA SUBUNIT.
 GN SFAD.
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_Taxid=5072;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Rosen S., Yu J.-H., Adams T.H.;
 RT "Aspergillus nidulans flba suppressor sfad identifies the G-beta
 subunit of a heterotrimeric G protein."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF056182; AAC3436.1; -;
 DR HSSP: P04901; ITBG.
 DR InterPro: IPR001632; -;
 DR InterPro: IPR001680; -;
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINBPT.
 DR PROSITE: PS00678; WD_REPEATS; UNKNOWN_3.
 DR SMART: SM00320; WD40; 1.
 KW Repeat, WD repeat.
 SQ SEQUENCE 352 AA; 38888 MW; 186A16886B4DF466 CRC64;

Query Match 67.2%; Score 1215.5; DB 3; Length 352;
 Best Local Similarity 64.6%; Pred. No. 1.7e-103;
 Matches 223; Conservative 48; Mismatches 67; Indels 7; Gaps 3;

QY 2 GEMEQIK-----QEADQLKQIADARKACADITLAEVSG-LEVYGRVOMRTTRTLGHL 55
 DB 6 GEMQAKITAAAREAEGLDKIRRRKDLADYTLRDVAQONQDAPRIGMKERRTLGHL 65
 QY 56 AKTYAMHWATDSKLIYASODGKLIWDTYTNKVHAIPLRSSVMWTCAYAPSGNPFACG 115
 DB 66 AKTYAMHWATDSKLIYASODGKLIWDTYTNKVHAIPLRSSVMWTCAYAPSGNPFACG 125
 QY 116 GLDNMCSIYLSKREGNVKVSRELTAHTGYLSCCRFLDNNIYVSGDTTCALMDETGO 175
 DB 126 GLDNMCSIYLSKREGNVKVSRELTAHTGYLSCCRFLDNNIYVSGDTTCALMDETGO 185
 QY 176 QKTFEYGHGDCMSLAVSP-DYKLFISGACDASAKIMDVREGTCROTFTGHESDINACF 234
 DB 186 KYTEFADHGDVMSISINPTNIFVSGADDAFAKIMDIRIGSVQTFAGHESDINACF 245
 QY 235 FPGNGEALCTGSDINACFPNGEALCTGSDINACFPNGEALCTGSDINACF 294
 DB 246 FPGNGEALCTGSDINACFPNGEALCTGSDINACFPNGEALCTGSDINACF 305
 QY 295 NVWDSLKCEKRVGLSGHNRVSCGLVADGMAVATGSDMSFLKLN 339
 DB 306 KVMWDLGNRVGSLSGHNRVSCGLVADGMAVATGSDMSFLKLN 350

RESULT 9
 09W3J1 PRELIMINARY; PRT; 358 AA.

AC 09W3J1
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE CG10763 PROTEIN.
 GN CG10763.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.-H.C., Yandell M.D., Zhang O., Chen L.X.,
 RA Brandon K.C., Rogers Y.-R.C., Blazer R.G., Chape M., Pfeiffer B.D.,
 RA Kian R., Doyle C., Baxter E.G., Helt C., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Giodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harits N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshnell A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissendach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AF003443; AAF46336.1; -.
 DR HSSP: P04901; 1786.
 DR Flybase: FBgn0030011; CG10763.
 DR InterPro: IPR001632; -.
 DR InterPro: IPR001680; -.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINB.
 DR PROSITE: PS00678; WD_REPEATS; 3.
 DR SMART: SM00320; WD40; 1.
 DR Repeat: WD repeat.
 SQ SEQUENCE 358 AA; 39354 MW; E9C6DEF91C503231 CRC64;

Query Match 52.9%; Score 957.5; DB 5; Length 358;
 Best Local Similarity 49.1%; Pred. No. 8.3e-80;
 Matches 167; Conservative 78; Mismatches 92; Indels 3; Gaps 2;
 QY 3 EMOGLQEAOLKQJADAKKACADITTLAELVSGLEVGRVQMTTRTLRGHLAKIYAMH 62
 DB 18 KMASTLVRENEKTKLEEROKLINDVNLINIAERLEQIAYVNIKRKYLKHQAKVLCCTD 77
 QY 63 WATDSKLIVASASODKLIYMDYTTNNKVAIPLRSSWMTCAVAPSGNFVACGGIDMNC 122
 DB 78 WSPDKRHIISSQDGLIITWDAFTTNKEHVAITPPTWMAACAVAPSGNFVACGGIDMNC 137
 QY 123 IYSLKRECVNVAVRELSAHTGYLSGCCRLD-DNNIVTSSGDTTCALMDIETGQOKYFV 181
 DB 138 VYPTTSDDEMAAKKRTVGHHTSYMSCIYPSNDQILILGSGDSTCALMDVSSGQLLOS 197
 QY 182 GHTGDCMSLAVPDY--KLFTSGACDASAKLMDVREGTCRGTFTGHESDINAICTFPNGE 239
 DB 198 GHSQGVMAIDLAPNETGTFTVSGSCDRNAFTWDMNSGIVVQSPFGHOSDVNSVAFHPCGD 257
 QY 240 AICTSSDASCRFLDRLADQELTAYSHESIIGITSAFSLGRLFAGYDDFCNCNWD 299
 DB 258 AATGSSDSSCRFLYMDRAREVAVFAKESITIFGVNSVDFSVSGLLFAGINDYTNLMDT 317
 QY 300 LKCEVGVLSGHNKRVSCIGVTADGMAVATGSMDSFLKIM 339
 DB 318 LKSERVCLLYGHNKRVSCVGVSPDGTALSTGSDWYTLRW 357

RESULT 10
 Q9HAY9 PRELIMINARY; PRT; 395 AA.
 ID Q9HAY9
 AC Q9HAY9
 DT 01-MAR-2001 (Tremblrel, 16, Created)
 DT 01-MAR-2001 (Tremblrel, 15, last sequence update)
 DT 01-MAR-2001 (Tremblrel, 16, last annotation update)
 DE GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT 5L.
 GN GNB5
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Puhl H.L., Ili Ikeda S.R., Aronstam R.S.;
 RT "Cloning and characterization of human G-protein beta 5L subunit."
 RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF300650; AAG18444.1; -.
 SQ SEQUENCE 395 AA; 43566 MW; E01B07CFCA587AD CRC64;

Query Match 52.3%; Score 946.5; DB 4; Length 395;
 Best Local Similarity 51.9%; Pred. No. 9.6e-79;
 Matches 177; Conservative 56; Mismatches 103; Indels 5; Gaps 3;
 QY 4 MBOLKQEAOLKQJADAKKACADITTLAELVSGLEVGRVQMTTRTLRGHLAKIYAMH 63
 DB 54 IASLSEAESLJKLEERAKLHYELHQAEREAQFVMTTRTLRGHLAKIYAMH 113
 QY 64 ATDSKLIVASASODKLIYMDYTTNNKVAIPLRSSWMTCAVAPSGNFVACGGIDMNC 123
 DB 114 CKDKRRIVSSQDGLIITWDAFTTNKEHVAITPPTWMAACAVAPSGNFVACGGIDMNC 173
 QY 124 YSL--KSRGCVNVAVRELSAHTGYLSGCCRLD-DNNIVTSSGDTTCALMDIETGQOKYF 180
 DB 174 YPLTFDKNENNAKAKKRVAMHTNLISACSTNSDMOILTAASGGTCALMDVSSGQLLOS 233
 QY 181 VGHFGD--CMSLAVSPDYKLFISGACDASAKLMDVREGTCRGTFTGHESDINAICTFPNG 238
 DB 234 HGHGADVLCDLAPSETGTGTFVSGGCDKRAMVDMNSGCGVAFHESDINAICTFPNG 293
 QY 239 EAITGSDASCRFLDRLADQELTAYSHESIIGITSAFSLGRLFAGYDDFCNCNWD 298
 DB 294 DARASGDDATCYLMDRAREVAVTAKESITIFGASVDFSLGRLFAGYDDYTNVMD 353
 QY 299 SLKCEVGVLSGHNKRVSCIGVTADGMAVATGSMDSFLKIM 339
 DB 354 VLKGRVSLIFGHNKRVSTLRVSPDGTALSTGSDWYTLRW 394

RESULT 11
 Q9NFZ1 PRELIMINARY; PRT; 346 AA.
 ID Q9NFZ1
 AC Q9NFZ1
 DT 01-OCT-2000 (Tremblrel, 15, Created)
 DT 01-OCT-2000 (Tremblrel, 15, last sequence update)
 DT 01-MAR-2001 (Tremblrel, 16, last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.
 OS Calliphora vicina (blue blowfly) (Calliphora erythrocephala).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
 OC Oestroidea; Calliphoridae; Calliphora.
 ON NCBI_TaxID=7373;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Schulz S., Huber A., Schwab K., Paulsen R.;
 RC TISSUE-EYE;
 RT "A novel gamma subunit of the fly compound eye."
 RT Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ250442; CAB76452.1; -.
 DR InterPro: IPR000364; -.

Db 179 QTCVMDITTTGLRTSVFGGFGSHTADVLISINSNGSLFVSGCDATARLMDTRVAS 238
 QY 218 -CROFTTGHESDINACEFPGNGEALICGSDASCRFLPADDELTAYS---HESIICCI 273
 Db 239 RAVRFHGHEDGVNSVKKFFPDGNGRFGSGEDGCRFLFDITGHQLOVYNOQHDNMAIV 298
 QY 274 TSVASTSLGRLFFAGYDDFNCNVWDSLKCRV---GVLSGHNRRSCGATADGMAVAT 329
 Db 299 TSIASISIGRLLIAGTYNGDCYVMDTLAVYLNLSLONSHEGRITTCGMSADGSACT 358
 QY 330 GSWDSFLKIM 339
 Db 359 GSWDTNLIKIM 368

RESULT 14
 Q9VW29 PRELIMINARY: PRT: 346 AA.
 AC Q9VW29;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 GN G-BETA-76C OR G-BETA-76C OR CG8770.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari P., Brottler P.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Bultman S.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos K., Delcher A., Deng Z., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mobergerson D.,
 RA Merkulov G., Mishina N.V., Murphy C., Morris J., Mostreli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.D.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein M., Strong R., Sun E.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: A003516; AAF49124.1; -;
 DR HSPD: P04901; ITBG.

DR FlyBase; FBgn0004623; G-beta-76C.
 DR InterPro; IPR001632; -;
 DR InterPro; IPR001680; -;
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00320; WD40; 1.
 KW Repeat; WD repeat.
 SO SEQUENCE 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match
 Best Local Similarity 45.5%; Score 823; DB 5; Length 346;
 Matches 147; Conservative 79; Mismatches 111; Indels 2; Gaps 1;
 QY 3 EMEOLKQAEOLKROIDARKACADITLAEVSGLEVGVHGVQMRRLRGLAKIYAMH 62
 Db 7 ETOKLYDEINGMIGKFPDDKSKADCTLDKCGMDGVPRKIFRFSKILKIHKNVSVH 66
 QY 63 WATDSKLLVSAOSDGLIWDYTTNKVNAIPLRSSVWATCAVPSGPNVACGGIDNACS 122
 Db 67 FAGDSRHCVTGSLDGLKLIWDYTTANKVOIPLRSAMVWTVAFSGNPFACGGIDNCT 126
 QY 123 IYLSKRE--GNVKSRELSAHTGYLSCCRFLDNNITYTSQDTTCALMDIETGQAKTVE 180
 Db 127 VYDVNRRDASGVAKMKVKELMGVEFLSCRFIDGHLITGSGDKMICHMDELKGVKTMD 186
 QY 181 VGHGDCMSLAVSPDYKLTISGACASAKLMDVREGTCRQFTGHESDINACEFPGNGE 240
 Db 187 NGRAGDAGLSLSPDMKTYITGSDVKTAKLMDVREGHKQFPHMDVSVCHHSFGG 246
 QY 241 ICGSDASCRFLPADDELTAYSHESIIIGTSVAFSLGRLFFAGYDDFNCNVWDSLT 300
 Db 247 FASCSDEQFARYMDLRADQIAQVPPPKNKGFTSCALSTSGRYLMCGIEGVHSDMTM 306
 QY 301 KCRVAVTSGHNRRSCGATADGMAVATGSMDSFLKIM 339
 Db 307 KORHGTGSHENRITCISLCPNGMCCLASTSMDQVRLW 345

RESULT 15
 Q9FV61 PRELIMINARY: PRT: 377 AA.
 AC Q9FV61;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 GN HETEROLOGIC GTP-BINDING PROTEIN SUBUNIT BETA 1.
 OS Nicotiana glauca (Common tobacco).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV; SAMSUN; TISSUE-HAIRY ROOT;
 RX MEDLINE=21002315; PubMed=11126570;
 RA Ando S., Takumi S., Ueda Y., Ueda T., Mori N., Nakamura C.;
 RT "Nicotiana glauca cDNAs encoding alpha and beta subunits of a
 RT heterologous GTP-binding protein isolated from hairy root tissues.";
 RL Genes Genet. Syst. 75:211-221(2000).
 DR EMBL: AF249743; ABG12330.1; -;
 SO SEQUENCE 377 AA; 40914 MW; 7052089F40A1707E CRC64;

Query Match
 Best Local Similarity 44.8%; Score 811; DB 10; Length 377;
 Matches 161; Conservative 71; Mismatches 99; Indels 26; Gaps 9;
 QY 4 MEOLKQAEOLKROIDARKACADITLAEVSGLEV--GRVQMRRLRGLAKIYAM 61
 Db 17 VNDLREKIKORQLD-----TDSVSGYARSGKTPVTGTPDIDVCCRILOGHTGKVSYL 71

Fri Sep 28 10:45:10 2001

us-09-492-029-3.rsp

Page 8

[illegible]

Search completed: September 28, 2001, 10:34:06
job time: 281 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 28, 2001, 10:28:49 ; Search time 25.94 Seconds
(without alignments)
998.433 Million cell updates/sec

Title: US-09-492-029-3
Perfect score: 1809
Sequence: 1 MGEMEQLKQAEQKQAD.....TADGMAVATGSDSFLKTN 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_68:
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1809	100.0	340	2 I53871	G-protein beta-sub
2	1762	97.4	340	1 RGHUB3	GTP-binding regula
3	1573	87.0	340	1 RGHUB1	GTP-binding regula
4	1573	87.0	340	1 RGHOB1	GTP-binding regula
5	1573	87.0	340	2 JC5057	G protein beta 1 -
6	1523	84.2	340	2 RGHUB2	GTP-binding regula
7	1520	84.0	340	2 T20830	hypothetical prote
8	1515	83.7	340	1 RGHUB	GTP-binding regula
9	1493	82.5	340	1 RGHUBA	GTP-binding regula
10	1482	81.9	341	2 RGHOB2	GTP-binding regula
11	1467	81.1	341	1 RGHOB2	GTP-binding regula
12	1467	81.1	341	1 RGHOB2	GTP-binding regula
13	1452	80.3	340	1 RGHOB1	GTP-binding regula
14	1225	67.7	347	2 A47370	GTP-binding regula
15	945.5	52.3	353	2 A54969	beta-5 GTP-binding
16	939.5	51.9	356	2 T22478	hypothetical prote
17	844	46.7	380	2 T03765	GTP-binding regula
18	828	45.8	380	2 T02085	GTP-binding regula
19	827	45.7	377	2 T03765	GTP-binding regula
20	826	45.7	346	1 RGHOB	GTP-binding regula
21	826	45.7	375	2 T03256	GTP-binding regula
22	826	45.7	377	2 T04086	GTP-binding protei
23	825	45.6	377	2 T04089	GTP-binding protei
24	817	45.2	377	2 T05266	GTP-binding regula
25	794	43.9	380	2 T08036	GTP-binding regula
26	792	43.8	377	2 T16985	GTP-binding protei
27	739.5	40.9	283	2 T12256	hypothetical prote
28	664	36.7	317	2 S72457	GTP-binding regula
29	663	36.7	305	2 T50474	GTP-binding regula

30	635	35.1	423	2 S60939	GTP-binding protei
31	601	33.2	123	2 S29121	GTP-binding regula
32	592.5	32.8	240	2 T02059	GTP-binding regula
33	383.5	21.2	1356	2 T18521	beta transducin-1i
34	310	17.1	1049	2 T42045	beta transducin-1i
35	308	17.0	333	2 G85034	probable WD-repeat
36	305.5	16.9	465	2 A32569	U4/U6 snRNP 52k pr
37	305	16.9	502	2 T41148	trp-asp repeat con
38	297.5	16.4	317	2 A33928	GTP-binding protei
39	297.5	16.4	317	2 B33928	GTP-binding protei
40	297.5	16.4	317	2 S45054	GTP-binding regula
41	297.5	16.4	317	2 S38398	GTP-binding regula
42	297.5	16.4	317	2 A36986	GTP-binding regula
43	295.5	16.3	586	2 T38992	activated protein
44	295	16.3	704	2 S33263	WD-40 repeat regul
45	294	16.3	554	2 T02445	transcription init
					probable U4/U6 sma

ALIGNMENTS

RESULT 1
I53871
G-protein beta-subunit - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C:Accession: I53871
R:Key: K. Robishaw, J.D.
Gene 149, 337-340, 1994
A:Title: Cloning and sequencing of a rat heart cDNA encoding a G-protein beta subunit
A:Reference number: I53871; M01D:95047499
A:Accession: I53871
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-340 <RES>
A:Cross-references: GB:129090; NID:9456703; PIDN:AAA62620.1; PID:9456704
A:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
F:222-255/Domain: WD repeat homology <WDR>

Query Match	100.0%; Score 1809; DB 2; Length 340;
Best Local Similarity	100.0%; Pred. No. 2.2e-142;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 MGEMEQLKQAEQKQADITTAELVSGLEVGRVOMFRRLRGLAKIYA 60
DB	1 MGEMEQLKQAEQKQADITTAELVSGLEVGRVOMFRRLRGLAKIYA 60
OY	61 MHMWDSTKLIVASASODGKLIYMDITTKVHAIPLRSSWMTCAVAPSGNFVACGGLDNK 120
DB	61 MHMWDSTKLIVASASODGKLIYMDITTKVHAIPLRSSWMTCAVAPSGNFVACGGLDNK 120
OY	121 CSTYLSIKRREGNVKYSRELASHTGYLSCCRFLDNNITVSSGDTTCALMDIEGQOKTVF 180
DB	121 CSTYLSIKRREGNVKYSRELASHTGYLSCCRFLDNNITVSSGDTTCALMDIEGQOKTVF 180
OY	181 VGHGTGCMKLANSPYKLFISGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
DB	181 VGHGTGCMKLANSPYKLFISGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
OY	241 ICGSPDASCRFLDLADDELTAHSHESITIGTISVAFSLGRLIFAGYDFFNNGWDSL 300
DB	241 ICGSPDASCRFLDLADDELTAHSHESITIGTISVAFSLGRLIFAGYDFFNNGWDSL 300
OY	301 KCRVGVLSGHDNRVSCIGTADGMAVATGSDSFLKTN 340
DB	301 KCRVGVLSGHDNRVSCIGTADGMAVATGSDSFLKTN 340

RESULT 2
RGHUB3
GTP-binding regulatory protein beta-3 chain - human
N:Alternate names: guanine nucleotide binding protein beta-3 chain; heterotrimeric G-

C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: A35096
 R:Levine, M.A.; Smallwood, P.M.; Moen Jr., P.T.; Helman, L.J.; Ahn, T.G.
 A:Title: Molecular cloning of beta3 subunit, a third form of the G protein beta-subunit
 A:Reference number: A35096; MUID:90192801
 A:Accession: A35096
 A:Molecule type: mRNA
 A:Residues: 1-340 <LEV>
 A:Cross-references: GB:M31328; NID:9183412; PIDN:AAA52582.1; PID:9306776
 C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
 rates. The beta and gamma chains, required for GTPase activity, appear to be common to all
 C:Comment: In mammals, four distinct types of beta chains have been found.
 C:Genetics:
 A:Gene: GDB:GNB3
 A:Cross-references: GDB:120005; OMIM:139130
 A:Map position: 12p13-12p13
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F:51-84/Domain: WD repeat homology <WD1>
 F:88-126/Domain: WD repeat homology <WD2>
 F:139-171/Domain: WD repeat homology <WD3>
 F:180-213/Domain: WD repeat homology <WD4>
 F:222-255/Domain: WD repeat homology <WD5>
 F:263-299/Domain: WD repeat homology <WD6>
 F:308-340/Domain: WD repeat homology <WD7>

Query Match
 Best Local Similarity 97.44; Score 1762; DB 1; Length 340;
 Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

1 MGEMEQLEKQAEQKQADITLAEVSGLEVGRVQMTTRTLRGHLAKIYA 60
 1 MGEHQLEKQAEQKQADITLAEVSGLEVGRVQMTTRTLRGHLAKIYA 60
 61 MHNATDSKLLVSAQODKLYMDTYTNNKVAIPLRSSWMTCAVPSGNFYACGLDM 120
 61 MHNATDSKLLVSAQODKLYMDTYTNNKVAIPLRSSWMTCAVPSGNFYACGLDM 120
 121 CSYSLKSRGKGVNSRELTAHTGYLSGCRFLDNNITVSSGDTTCALMDITGQOKTFF 180
 121 CSYSLKSRGKGVNSRELTAHTGYLSGCRFLDNNITVSSGDTTCALMDITGQOKTFF 180
 181 VGHGDCMSLAASPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACFPNGEA 240
 181 VGHGDCMSLAASPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACFPNGEA 240
 241 ICHGSDASCRFLDLRADDELTAHSHESITIGITVAFLSGRLFAGYDDPNCVWDSL 300
 241 ICHGSDASCRFLDLRADDELTAHSHESITIGITVAFLSGRLFAGYDDPNCVWDSL 300
 301 KCEKRVGLSGHNRVSCGLVTDGMAVATGWSDFLKIWN 340
 301 KCEKRVGLSGHNRVSCGLVTDGMAVATGWSDFLKIWN 340

RESULT 3
 RGH0B1
 N:Alternate names: guanine nucleotide binding protein beta-1 chain; heterotrimeric G-pro
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: A24853
 R:Codina, J.; Stengel, D.; Woo, S.L.C.; Birnbaumer, L.
 A:Title: Beta-subunits of the human liver Gs/Gi signal-transducing proteins and those of
 A:Reference number: A91368; MUID:87030912
 A:Accession: A24853
 A:Molecule type: mRNA
 A:Residues: 1-340 <COD>

A:Cross-references: GB:X04526; NID:931667; PIDN:CAA28207.1; PID:931669
 A:Experimental source: Liver
 A:Note: The authors translated the codon GAG for residues 138 and 172 as Gln
 C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
 rates. The beta and gamma chains, required for GTPase activity, appear to be common to
 C:Comment: In mammals, four distinct types of beta chains have been found.
 C:Genetics:
 A:Gene: GDB:GNB1
 A:Cross-references: GDB:119279; OMIM:139380
 A:Map position: 1p36-1p31.2
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F:51-84/Domain: WD repeat homology <WD1>
 F:88-126/Domain: WD repeat homology <WD2>
 F:139-171/Domain: WD repeat homology <WD3>
 F:180-213/Domain: WD repeat homology <WD4>
 F:222-255/Domain: WD repeat homology <WD5>
 F:263-299/Domain: WD repeat homology <WD6>
 F:308-340/Domain: WD repeat homology <WD7>

Query Match
 Best Local Similarity 87.08; Score 1573; DB 1; Length 340;
 Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;

1 MGEMEQLEKQAEQKQADITLAEVSGLEVGRVQMTTRTLRGHLAKIYA 60
 1 MSELQLEKQAEQKQADITLAEVSGLEVGRVQMTTRTLRGHLAKIYA 60
 61 MHNATDSKLLVSAQODKLYMDTYTNNKVAIPLRSSWMTCAVPSGNFYACGLDM 120
 61 MHNATDSKLLVSAQODKLYMDTYTNNKVAIPLRSSWMTCAVPSGNFYACGLDM 120
 121 CSYSLKSRGKGVNSRELTAHTGYLSGCRFLDNNITVSSGDTTCALMDITGQOKTFF 180
 121 CSYSLKSRGKGVNSRELTAHTGYLSGCRFLDNNITVSSGDTTCALMDITGQOKTFF 180
 181 VGHGDCMSLAASPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACFPNGEA 240
 181 VGHGDCMSLAASPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACFPNGEA 240
 241 ICHGSDASCRFLDLRADDELTAHSHESITIGITVAFLSGRLFAGYDDPNCVWDSL 300
 241 ICHGSDASCRFLDLRADDELTAHSHESITIGITVAFLSGRLFAGYDDPNCVWDSL 300
 301 KCEKRVGLSGHNRVSCGLVTDGMAVATGWSDFLKIWN 340
 301 KCEKRVGLSGHNRVSCGLVTDGMAVATGWSDFLKIWN 340

RESULT 4
 RGH0B1
 N:Alternate names: guanine nucleotide binding protein beta-1 chain; heterotrimeric G-
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: A24225
 R:Sugimoto, K.; Nakada, T.; Tanabe, T.; Takahashi, H.; Noda, M.; Minamino, N.; Kangaw
 A:Title: Primary structure of the beta-subunit of bovine transducin deduced from the
 A:Reference number: A24225; MUID:86030675
 A:Accession: A24225
 A:Molecule type: mRNA
 A:Residues: 1-340 <SUG>
 A:Cross-references: GB:X03073
 R:Fong, H.K.W.; Hurlley, J.B.; Hopkins, R.S.; Maize-Lye, R.; Johnson, M.S.; Doolittle,
 Proc. Natl. Acad. Sci. U.S.A. 83, 2162-2166, 1986
 A:Title: Repetitive segmental structure of the transducin beta subunit: homology with
 A:Reference number: A25457; MUID:86177563
 A:Accession: A25457
 A:Molecule type: mRNA
 A:Residues: 1-340 <FON>

A:Cross-references: GB:M13236; NID:g163782; PIDN:AAA03792.1; PID:g163783
 C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
 the beta and gamma chains, required for GTPase activity, appear to be common to all
 rats. It is specific for each type of G protein.
 C:Comment: In mammals, four distinct types of beta chains have been found.
 C:Keywords: GTP binding; heterotrimer; signal transduction
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F:1-84/Domain: WD repeat homology <WD1>
 F:88-126/Domain: WD repeat homology <WD2>
 F:139-171/Domain: WD repeat homology <WD3>
 F:180-213/Domain: WD repeat homology <WD4>
 F:222-255/Domain: WD repeat homology <WD5>
 F:263-299/Domain: WD repeat homology <WD6>
 F:308-340/Domain: WD repeat homology <WD7>

Query Match 87.0%; Score 1573; DB 1; Length 340;
 Best Local Similarity 83.2%; Pred. No. 7.9e-123; Indels 0; Gaps 0;
 Matches 283; Conservative 31; Mismatches 26;

QY 1 MGEHOLKOEADOLKQIADARACADITLAEVSGLEVGRVQMTFRRLRGLAKIYA 60
 1 MSELDOLEADOLKQIADARACADITLAEVSGLEVGRVQMTFRRLRGLAKIYA 60
 Db 1 MSELDOLEADOLKQIADARACADITLAEVSGLEVGRVQMTFRRLRGLAKIYA 60
 QY 61 MHWATDSKLIVASASODGKLIWDTYTTNKVAIPLRSSVWMTCAVPSGNFVACGGLDN 120
 61 MHWATDSKLIVASASODGKLIWDTYTTNKVAIPLRSSVWMTCAVPSGNFVACGGLDN 120
 Db 61 MHWATDSKLIVASASODGKLIWDTYTTNKVAIPLRSSVWMTCAVPSGNFVACGGLDN 120
 QY 121 CSYISLKRREGNVKVSRELHAGTGLSCRFDDNNITVSSGDTTCALMDITGQQTTF 180
 121 CSYISLKRREGNVKVSRELHAGTGLSCRFDDNNITVSSGDTTCALMDITGQQTTF 180
 Db 121 CSYISLKRREGNVKVSRELHAGTGLSCRFDDNNITVSSGDTTCALMDITGQQTTF 180
 QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 240
 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 240
 Db 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 240
 QY 241 TGHGTGVMSLSLADPTLRFVSGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 300
 241 TGHGTGVMSLSLADPTLRFVSGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 300
 Db 241 TGHGTGVMSLSLADPTLRFVSGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 300
 QY 301 KCEKRVGLSGHDMRVSCIGVADGMAVATGSMDSFLKIN 340
 301 KCEKRVGLSGHDMRVSCIGVADGMAVATGSMDSFLKIN 340
 Db 301 KCEKRVGLSGHDMRVSCIGVADGMAVATGSMDSFLKIN 340

RESULT 5
 JC5057
 G protein beta 1 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Aug-1999
 C:Accession: JC5057
 R:Qin R.; Schlimer, B.P.
 Gene 175, 275-277, 1996
 A:Title: cDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins
 A:Reference number: JC5057; MUID:97074684
 A:Accession: JC5057
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-340 <QIU>
 A:Cross-references: GB:U29055; NID:g868168; PIDN:AAC52905.1; PID:g868169
 A:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 C:Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory he
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F:1-84/Domain: WD repeat homology <WD1>
 F:88-126/Domain: WD repeat homology <WD2>
 F:139-171/Domain: WD repeat homology <WD3>
 F:180-213/Domain: WD repeat homology <WD4>
 F:222-255/Domain: WD repeat homology <WD5>
 F:263-299/Domain: WD repeat homology <WD6>
 F:308-340/Domain: WD repeat homology #status atypical <WD7>

Query Match 87.0%; Score 1573; DB 2; Length 340;
 Best Local Similarity 83.2%; Pred. No. 7.9e-123;

Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;

QY 1 MGEHOLKOEADOLKQIADARACADITLAEVSGLEVGRVQMTFRRLRGLAKIYA 60
 1 MSELDOLEADOLKQIADARACADITLAEVSGLEVGRVQMTFRRLRGLAKIYA 60
 Db 1 MSELDOLEADOLKQIADARACADITLAEVSGLEVGRVQMTFRRLRGLAKIYA 60
 QY 61 MHWATDSKLIVASASODGKLIWDTYTTNKVAIPLRSSVWMTCAVPSGNFVACGGLDN 120
 61 MHWATDSKLIVASASODGKLIWDTYTTNKVAIPLRSSVWMTCAVPSGNFVACGGLDN 120
 Db 61 MHWATDSKLIVASASODGKLIWDTYTTNKVAIPLRSSVWMTCAVPSGNFVACGGLDN 120
 QY 121 CSYISLKRREGNVKVSRELHAGTGLSCRFDDNNITVSSGDTTCALMDITGQQTTF 180
 121 CSYISLKRREGNVKVSRELHAGTGLSCRFDDNNITVSSGDTTCALMDITGQQTTF 180
 Db 121 CSYISLKRREGNVKVSRELHAGTGLSCRFDDNNITVSSGDTTCALMDITGQQTTF 180
 QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 240
 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 240
 Db 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 240
 QY 241 TGHGTGVMSLSLADPTLRFVSGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 300
 241 TGHGTGVMSLSLADPTLRFVSGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 300
 Db 241 TGHGTGVMSLSLADPTLRFVSGACDASAKIMDVREMGKQFTGHESDINAIICEFPNGEA 300
 QY 301 KCEKRVGLSGHDMRVSCIGVADGMAVATGSMDSFLKIN 340
 301 KCEKRVGLSGHDMRVSCIGVADGMAVATGSMDSFLKIN 340
 Db 301 KCEKRVGLSGHDMRVSCIGVADGMAVATGSMDSFLKIN 340

RESULT 6
 GDB02
 GTP-binding regulatory protein beta-2 chain - human
 N:Alternate names: guanine nucleotide binding protein beta-2 chain; heterotrimeric G-
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: B26617; B28040
 R:Hong H.K.W.; Amatruda III, T.T.; Birren, B.W.; Simon, M.I.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6122-6125, 1987
 A:Title: Distinct forms of the beta-subunit of GTP-binding regulatory proteins ident
 A:Reference number: A94155; MUID:87231903
 A:Accession: B26617
 A:Molecule type: mRNA
 A:Residues: 1-340 <PON>
 A:Cross-references: GB:M16514; NID:g183469; PIDN:AAA03179.1; PID:g386751
 R:Gao, B.; Gilman, A.G.; Robishaw, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6122-6125, 1987
 A:Title: A second form of the beta subunit of signal-transducing G proteins.
 A:Reference number: A94177; MUID:87317607
 A:Accession: B28040
 A:Molecule type: mRNA
 A:Residues: 1-340 <GAO>
 A:Cross-references: GB:M16538
 C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
 the beta and gamma chains, required for GTPase activity, appear to be common to
 rats. It is specific for each type of G protein.
 C:Comment: In mammals, four distinct types of beta chains have been found.
 C:Genetics:
 A:Gene: GDB:GDB2
 A:Cross-references: GDB:120004; OMIM:139390
 A:Map position: 7q21.3-7q22.1
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 C:Keywords: GTP binding; heterotrimer; signal transduction
 F:1-84/Domain: WD repeat homology <WD1>
 F:88-126/Domain: WD repeat homology <WD2>
 F:139-171/Domain: WD repeat homology <WD3>
 F:180-213/Domain: WD repeat homology <WD4>
 F:222-255/Domain: WD repeat homology <WD5>
 F:263-299/Domain: WD repeat homology <WD6>
 F:308-340/Domain: WD repeat homology <WD7>

Query Match 84.2%; Score 1523; DB 1; Length 340;
 Best Local Similarity 80.9%; Pred. No. 1.1e-118;
 Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

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QY 1 MGEBOUKOEAEOIKQIADARACADITLAEVSGLEVGVQVQRTTRRLRGLAKIYA 60
   1 MSELDOLOREAEOIKQIADARACADITLAEVSGLEVGVQVQRTTRRLRGLAKIYA 60
Db 1 MSELDOLOREAEOIKQIADARACADITLAEVSGLEVGVQVQRTTRRLRGLAKIYA 60
QY 61 MHWATDSKLLVSAOSQDKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
   61 MHWATDSKLLVSAOSQDKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
Db 61 MHWATDSKLLVSAOSQDKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
QY 121 CSTYLSKREGNVKVSRELSTAGTGLSCRFDDNNIYSSGDTTCALMDIETGQOQTVF 180
   121 CSTYLSKREGNVKVSRELSTAGTGLSCRFDDNNIYSSGDTTCALMDIETGQOQTVF 180
Db 121 CSTYLSKREGNVKVSRELSTAGTGLSCRFDDNNIYSSGDTTCALMDIETGQOQTVF 180
QY 181 VGHGTGCMASLPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAIQFPNGEA 240
   181 VGHGTGCMASLPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAIQFPNGEA 240
Db 181 VGHGTGCMASLPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAIQFPNGEA 240
QY 241 ICTGSDASCRFLDLRAOQELTAYSHESIIGITSVAFSLSGRLTFAGYDDFNCAWWSL 300
   241 ICTGSDASCRFLDLRAOQELTAYSHESIIGITSVAFSLSGRLTFAGYDDFNCAWWSL 300
Db 241 ICTGSDASCRFLDLRAOQELTAYSHESIIGITSVAFSLSGRLTFAGYDDFNCAWWSL 300
QY 301 KGERGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIWN 340
   301 KGERGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIWN 340
Db 301 KGERGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIWN 340

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RESULT 7

hypothetical protein F13D12.7 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T20830
 R:Colles, L.
 submitted to the EMBL Data Library, April 1995
 A:Reference number: T20830
 A:Accession: T20830
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-340 <Wtl>
 A:Cross-references: EMBL:Z49127; PIDN:CAA8948.1; GSPDB:GN00020; CESP:F13D12.7
 A:Experimental source: clone F13D12
 C:Genetics:
 A:Gene: CESP:F13D12.7
 A:Map position: 2
 A:Introns: 19/3; 57/3; 89/3; 116/2; 166/2; 209/3; 233/3; 306/1
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

Query Match
 Best Local Similarity 84.0%; Score 1520; DB 1; Length 340;
 Matches 276; Conservative 31; Mismatches 33; Indels 0; Gaps 0;

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QY 1 MGEBOUKOEAEOIKQIADARACADITLAEVSGLEVGVQVQRTTRRLRGLAKIYA 60
   1 MSELDOLOREAEOIKQIADARACADITLAEVSGLEVGVQVQRTTRRLRGLAKIYA 60
Db 1 MSELDOLOREAEOIKQIADARACADITLAEVSGLEVGVQVQRTTRRLRGLAKIYA 60
QY 61 MHWATDSKLLVSAOSQDKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
   61 MHWATDSKLLVSAOSQDKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
Db 61 MHWATDSKLLVSAOSQDKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
QY 121 CSTYLSKREGNVKVSRELSTAGTGLSCRFDDNNIYSSGDTTCALMDIETGQOQTVF 180
   121 CSTYLSKREGNVKVSRELSTAGTGLSCRFDDNNIYSSGDTTCALMDIETGQOQTVF 180
Db 121 CSTYLSKREGNVKVSRELSTAGTGLSCRFDDNNIYSSGDTTCALMDIETGQOQTVF 180
QY 181 VGHGTGCMASLPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAIQFPNGEA 240
   181 VGHGTGCMASLPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAIQFPNGEA 240
Db 181 VGHGTGCMASLPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAIQFPNGEA 240
QY 241 ICTGSDASCRFLDLRAOQELTAYSHESIIGITSVAFSLSGRLTFAGYDDFNCAWWSL 300
   241 ICTGSDASCRFLDLRAOQELTAYSHESIIGITSVAFSLSGRLTFAGYDDFNCAWWSL 300
Db 241 ICTGSDASCRFLDLRAOQELTAYSHESIIGITSVAFSLSGRLTFAGYDDFNCAWWSL 300
QY 301 KGERGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIWN 340
   301 KGERGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIWN 340

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Db 301 KGERGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIWN 340

RESULT 8

GTP-binding regulatory protein beta chain - *Caenorhabditis elegans*
 N:Alternate names: guanine nucleotide binding protein beta chain; heterotrimeric G-protein
 C:Species: *Caenorhabditis elegans*
 C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: S09591
 R:van der Voorn, L.; Gebbink, M.; Plasterk, R.H.A.; Ploegh, H.L.
 J. Mol. Biol. 213, 17-26, 1990
 A:Title: Characterization of a G-protein beta-subunit gene from the nematode *Caenorhabditis elegans*
 A:Reference number: S09591; MOID:90250769
 A:Accession: S09591
 A:Molecule type: DNA
 A:Residues: 1-340 <VAN>
 A:Cross-references: EMBL:X17497; NID:96642; PIDN:CAA3532.1; PID:96643
 C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that regulate the beta and gamma chains, required for GTPase activity, appear to be common to all eukaryotes.
 C:Comment: In mammals, four distinct types of beta chains have been found.
 A:Introns: 19/3; 57/3; 89/3; 115/2; 166/2; 209/3; 233/3; 305/2
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 C:Keywords: GTP binding; heterotrimer; signal transduction
 F:51-84/Domain: WD repeat homology <WD1>
 F:88-126/Domain: WD repeat homology <WD2>
 F:139-171/Domain: WD repeat homology <WD3>
 F:180-213/Domain: WD repeat homology <WD4>
 F:222-255/Domain: WD repeat homology <WD5>
 F:263-299/Domain: WD repeat homology <WD6>
 F:308-340/Domain: WD repeat homology <WD7>

Query Match

Best Local Similarity 83.7%; Score 1515; DB 1; Length 340;
 Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

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QY 1 MGEBOUKOEAEOIKQIADARACADITLAEVSGLEVGVQVQRTTRRLRGLAKIYA 60
   1 MSELDOLOREAEOIKQIADARACADITLAEVSGLEVGVQVQRTTRRLRGLAKIYA 60
Db 1 MSELDOLOREAEOIKQIADARACADITLAEVSGLEVGVQVQRTTRRLRGLAKIYA 60
QY 61 MHWATDSKLLVSAOSQDKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
   61 MHWATDSKLLVSAOSQDKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
Db 61 MHWATDSKLLVSAOSQDKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
QY 121 CSTYLSKREGNVKVSRELSTAGTGLSCRFDDNNIYSSGDTTCALMDIETGQOQTVF 180
   121 CSTYLSKREGNVKVSRELSTAGTGLSCRFDDNNIYSSGDTTCALMDIETGQOQTVF 180
Db 121 CSTYLSKREGNVKVSRELSTAGTGLSCRFDDNNIYSSGDTTCALMDIETGQOQTVF 180
QY 181 VGHGTGCMASLPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAIQFPNGEA 240
   181 VGHGTGCMASLPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAIQFPNGEA 240
Db 181 VGHGTGCMASLPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAIQFPNGEA 240
QY 241 ICTGSDASCRFLDLRAOQELTAYSHESIIGITSVAFSLSGRLTFAGYDDFNCAWWSL 300
   241 ICTGSDASCRFLDLRAOQELTAYSHESIIGITSVAFSLSGRLTFAGYDDFNCAWWSL 300
Db 241 ICTGSDASCRFLDLRAOQELTAYSHESIIGITSVAFSLSGRLTFAGYDDFNCAWWSL 300
QY 301 KGERGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIWN 340
   301 KGERGVLSGHDNRVSCLGVTADGMAVATGSMDSFLKIWN 340

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RESULT 9

GTP-binding regulatory protein beta-4 chain - mouse
 N:Alternate names: guanine nucleotide binding protein beta-4 chain; heterotrimeric G-protein
 C:Species: *Mus musculus* (house mouse)
 C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: J50669
 R:van Weizsacker, E.; Strathmann, M.P.; Simon, M.I.
 Biochem. Biophys. Res. Commun. 183, 350-356, 1992

Db 1 RNQIRDKAKACGSDTLTQITAGDIPVGRIQMTRRLRGLAKIYAMHMGDSRLLYAS 60
 QY 75 ODGLIYWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNMCSYLSKSEGNK 134
 Db 61 ODGLIYWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNMCSYLSKSEGNK 120
 QY 135 VSRSLAHHTGYLSCCRFLDDNNITVSSGDTTCALMDIETGOOKTFEVGHTGDCMLAVSP 194
 Db 121 VSRSLAHHTGYLSCCRFLDDNNITVSSGDTTCALMDIETGOOKTFEVGHTGDCMLAVSP 180
 QY 195 DYKLFISGACDASAKLMDYREGTQRTFGHSHSDINACFFPNGAICITGSDSACRLFD 254
 Db 181 DGHFTVSGACDASAKLMDYREGTQRTFGHSHSDINACFFPNGAICITGSDSACRLFD 240
 QY 255 LRADQELTAVSHESIIGTTSVAFSLSGRLTFAGYDDEFCNWDLSKCEERYVLSGHNH 314
 Db 241 LRADQELTAVSHESIIGTTSVAFSLSGRLTFAGYDDEFCNWDLSKCEERYVLSGHNH 300
 QY 315 VSLGVTADGMAVATGSMDSFLKIN 340
 Db 301 VSLGVTADGMAVATGSMDSFLKIN 326

RESULT 12

RGOOBR

GTP-binding regulatory protein beta chain - northern European squid
 N:Alternate names: guanine nucleotide binding protein beta chain; heterotrimeric G-protein
 C:Species: Lolligo forbesi (northern European squid)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: S13302
 R:Ryba, N.J.P.; Pottinger, J.D.D.; Keen, J.N.; Findlay, J.B.C.
 Biochem. J. 273, 225-228, 1991
 A:Title: Sequence of the beta subunit of the phosphatidylinositol-specific phospholipase
 A:Reference number: S13302; MUID:91113146
 A:Accession: S13302
 A:Molecule type: mRNA
 A:Residues: 1-341 <RYB>
 A:Cross-references: EMBL:X56757; NID:99507; PIRN:CAA0077.1; PTD:99508
 C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
 ans. The beta and gamma chains, required for GTPase activity, appear to be common to all
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 C:Keywords: GTP-binding; heterotrimer; signal transduction
 F:89-127/Domain: WD repeat homology <WD1>
 F:140-172/Domain: WD repeat homology <WD2>
 F:181-214/Domain: WD repeat homology <WD3>
 F:223-256/Domain: WD repeat homology <WD4>
 F:264-300/Domain: WD repeat homology <WD5>
 F:309-341/Domain: WD repeat homology <WD6>

Query Match 81.1%; Score 1467; DB 1; Length 341;
 Best Local Similarity 79.9%; Pred. No. 4.8e-114;

Matches 270; Conservative 30; Mismatches 38; Indels 0; Gaps 0;

QY 3 EMEQLQAEOLKQIADAKACADITLAEVSGLEVVGRVOMTRRLRGLAKIYAMH 62
 Db 4 ELRLRQETEQLNQIRKRAADPTLAMATANPEVRIMQRTKRLRGLAKIYAMH 63
 QY 63 WATDSKILVASODGKLIYWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNMCS 122
 Db 64 WATDSKILVASODGKLIYWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNMCS 123
 QY 123 IYSLKREGNVKYSRLSAHTGYLSCCRFLDDNNITVSSGDTTCALMDIETGOOKTFEVG 182
 Db 124 IYSLKREGNVKYSRLSAHTGYLSCCRFLDDNNITVSSGDTTCALMDIETGOOKTFEVG 183
 QY 183 HNGDCSLAVSPDYKLFISGACDASAKLMDYREGTQRTFGHSHSDINACFFPNGAIC 242
 Db 184 HNGDCSLAVSPDYKLFISGACDASAKLMDYREGTQRTFGHSHSDINACFFPNGAIC 243
 QY 243 TGSDDASCRFLRADQELTAVSHESIIGTTSVAFSLSGRLTFAGYDDEFCNWDLSK 302

Db 244 TGSDDATCRLFLRADQELTAVSHESIIGTTSVAFSGRLLGIDYDFNKNWVDYKQ 303
 QY 303 ERVGVLSGHDNRVSCGVTADGMAVATGSMDSFLKIN 340
 Db 304 ERVGVLSGHDNRVSCGVTADGMAVATGSMDSFLKIN 341

RESULT 13

RGEFBH

GTP-binding regulatory protein beta chain homolog - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: A40489
 R:Farfitt, S.; Provost, N.M.; Hurley, J.B.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7134-7138, 1988
 A:Title: Cloning of a Drosophila melanogaster guanine nucleotide regulatory protein b
 A:Reference number: A40489; MUID:89017152
 A:Accession: A40489
 A:Molecule type: mRNA
 A:Residues: 1-340 <YAR>
 A:Cross-references: GB:M22567; GB:J04083; NID:9157497; PIRN:AA859247.1; PTD:9157498
 C:Genetics:
 A:Gene: FlyBase:Gdbpr
 A:Cross-references: FlyBase:FBgn0001105
 A:Map position: X13F
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F:51-84/Domain: WD repeat homology <WD1>
 F:89-126/Domain: WD repeat homology <WD2>
 F:139-171/Domain: WD repeat homology <WD3>
 F:180-213/Domain: WD repeat homology <WD4>
 F:222-255/Domain: WD repeat homology <WD5>
 F:263-299/Domain: WD repeat homology <WD6>
 F:308-340/Domain: WD repeat homology <WD7>

Query Match 80.3%; Score 1452; DB 1; Length 340;
 Best Local Similarity 76.5%; Pred. No. 8.3e-113;

Matches 260; Conservative 38; Mismatches 42; Indels 0; Gaps 0;

QY 1 MGEMLQAEOLKQIADAKACADITLAEVSGLEVVGRVOMTRRLRGLAKIYAMH 60
 Db 1 MNEEDLSRQEAESLKNAIRAKACDPTSLQATSLDEPIGRQMTRRLRGLAKIYAMH 60
 QY 61 MHWATDSKILVASODGKLIYWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 Db 61 MHWATDSKILVASODGKLIYWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 QY 121 CSYLSKREGNVKYSRLSAHTGYLSCCRFLDDNNITVSSGDTTCALMDIETGOOKTFEV 180
 Db 121 CSYLSKREGNVKYSRLSAHTGYLSCCRFLDDNNITVSSGDTTCALMDIETGOOKTFEV 180
 QY 181 VGHGDCSLAVSPDYKLFISGACDASAKLMDYREGTQRTFGHSHSDINACFFPNGA 240
 Db 181 LGHTGVMAISLAPQCKTFVSGACDASAKLMDIETGOOKTFEVGHTGHSINAVTFPPNGA 240
 QY 241 IYSGSDATCRLFLRADQELTAVSHESIIGTTSVAFSLSGRLTFAGYDDEFCNWDLSK 300
 Db 241 FATGSDATCRLFLRADQELTAVSHESIIGTTSVAFSLSGRLTFAGYDDEFCNWDLSK 300
 QY 301 KCEERVVLSGHDNRVSCGVTADGMAVATGSMDSFLKIN 340
 Db 301 KAERSGILAGHDNRVSCGVTADGMAVATGSMDSFLKIN 340

RESULT 14

A47370

GTP-binding regulatory protein beta chain - slime mold (Dictyostellium discoideum)
 C:Species: Dictyostellium discoideum
 C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
 C:Accession: A47370
 R:Rilly, P.; Wu, L.; Welker, D.L.; Devreotes, P.N.
 Genes Dev. 7, 986-995, 1993

```

Query Match      52.3%  Score 945.5;  DB 2,  Length 353;
Best Local Similarity 51.6%  Pred. No. 8e-71;
Matches 176;  Conservative 57;  Mismatches 103;  Indels 5;  Gaps 3;

OY      4 MEDLKEAEGLKQIADARACADITLAEVLSGLEVGVRGMRKRRFLRGHLAKIYAMH 63
      :  || ||| || : :  |  | : : :  : : : :  | : ||||| : ||  |  |  |

```

Search completed: September 28, 2001, 10:33:20
Job time: 271 sec

Fri Sep 28 10:45:08 2001

us-09-492-029-3.rpt

Page 8

0
.
i

Fri Sep 28 10:45:11 2001

us-09-492-029-5.rag

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:29:21 ; Search time 34.79 seconds
(without alignments)
592.474 Million cell updates/sec

Title: US-09-492-029-5
Perfect score: 1809
Sequence: 1 MGEHQLRQEAQLKROLD.....TADGMAVATGSMDSFLKWN 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.GeneSeq_0601.*
1: /SID8/gcgdata/geneSeq/geneSeq/AA1980.DAT.*
2: /SID8/gcgdata/geneSeq/geneSeq/AA1981.DAT.*
3: /SID8/gcgdata/geneSeq/geneSeq/AA1982.DAT.*
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7: /SID8/gcgdata/geneSeq/geneSeq/AA1986.DAT.*
8: /SID8/gcgdata/geneSeq/geneSeq/AA1987.DAT.*
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19: /SID8/gcgdata/geneSeq/geneSeq/AA1998.DAT.*
20: /SID8/gcgdata/geneSeq/geneSeq/AA2000.DAT.*
21: /SID8/gcgdata/geneSeq/geneSeq/AA2001.DAT.*
22: /SID8/gcgdata/geneSeq/geneSeq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1809	100.0	340	AAW36598	Human G protein be
2	1809	100.0	340	AAW36598	Human G protein be
3	1809	100.0	340	AAW36598	Human G protein be
4	1807	99.9	340	AAW36598	Human G protein be
5	1806	99.8	340	AAW36598	Human G protein be
6	1806	99.8	340	AAW36598	Human G protein be
7	1765	97.6	340	AAW36598	Human G protein be
8	1762	97.4	340	AAW36598	Human G protein be
9	1759	97.2	340	AAW36598	Human G protein be
10	1758	97.2	340	AAW36598	Human G protein be
11	1578	87.2	340	AAW36598	Human G protein be

12	1578	87.2	340	AAW36598	Human G protein be
13	1578	86.2	299	AAW36598	Human G protein be
14	1548.5	85.6	297	AAW36598	Human G protein be
15	1528	84.5	340	AAW36598	Human G protein be
16	1528	84.5	340	AAW36598	Human G protein be
17	1500	82.9	340	AAW36598	Human G protein be
18	1463	80.9	341	AAW36598	Human G protein be
19	1459	80.7	340	AAW36598	Human G protein be
20	1421	78.6	340	AAW36598	Human G protein be
21	949.5	52.5	353	AAW36598	Human G protein be
22	948.5	50.1	353	AAW36598	Human G protein be
23	906.5	50.1	295	AAW36598	Human G protein be
24	868.5	48.0	295	AAW36598	Human G protein be
25	865.5	47.8	295	AAW36598	Human G protein be
26	815	45.1	377	AAW36598	Human G protein be
27	658.5	36.4	422	AAW36598	Human G protein be
28	650	35.9	422	AAW36598	Human G protein be
29	650	35.9	423	AAW36598	Human G protein be
30	650	35.9	423	AAW36598	Human G protein be
31	649	35.9	423	AAW36598	Human G protein be
32	647	35.7	422	AAW36598	Human G protein be
33	646	35.7	267	AAW36598	Human G protein be
34	645.5	35.7	267	AAW36598	Human G protein be
35	645.5	35.7	267	AAW36598	Human G protein be
36	612.5	33.9	225	AAW36598	Human G protein be
37	566	32.9	243	AAW36598	Human G protein be
38	566	31.4	166	AAW36598	Human G protein be
39	524	29.0	227	AAW36598	Human G protein be
40	524	29.0	227	AAW36598	Human G protein be
41	422.5	23.4	203	AAW36598	Human G protein be
42	308	17.0	333	AAW36598	Human G protein be
43	305.5	16.9	317	AAW36598	Human G protein be
44	305.5	16.9	317	AAW36598	Human G protein be
45	305.5	16.9	317	AAW36598	Human G protein be

ALIGNMENTS

RESULT 1	AAW36598	standard; Protein; 340 AA.
ID	AAW36598	standard; Protein; 340 AA.
AC	AAW36598	
DT	19-MAY-1998	(first entry)
DE	Human G protein beta-3 subunit.	
KW	G protein beta-3 subunit; variant; mutation; hypertension; diagnosis;	
OS	cardiovascular disease; metabolic disorder; immunological disorder.	
PN	Homo sapiens.	
PN	DE19619362-A1.	
PD	20-NOV-1997.	
PF	14-MAY-1996; 96DE-1019362.	
PR	14-MAY-1996; 96DE-1019362.	
PA	(BAD1) BASF AG.	
PI	Sifflert W;	
DR	WPI: 1998-000675/01.	
DR	N-PSDB: AAT96746; AAW09741.	
PT	Assessing risk of disease, especially hypertension - by detecting	
PS	mutation in human G-protein beta-3 sub:unit gene	
PS	Claim 3; Page 6; Bpp; German.	

XX This sequence represents the human G-protein beta 3 subunit. A variant
 CC of the gene encoding this protein has applications in the diagnosis of
 CC diseases or assessing the risk of a disease associated with G-protein
 CC misregulation. G-protein misregulation is associated with hypertension,
 CC cardiovascular diseases e.g. coronary heart disease, atherosclerosis,
 CC restenosis, stroke and thrombosis, metabolic disorders such as diabetes,
 CC diabetic complications, disorders of lipid metabolism and central
 CC chemoreceptor dysfunction (e.g. sudden infant death syndrome), and
 CC immunological disorders such as impaired wound healing, tumours, AIDS,
 CC cirrhosis and transplant rejection.

Sequence 340 AA;

Query Match 100.0%; Score 1809; DB 19; Length 340;
 Best Local Similarity 100.0%; Pred. No. 5.3e-171;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MGEMOLROEAEOLKQIADARACADVTTLAEVSGLEVGVOMRTTRTLRGLAKIYA 60
 1 mgemeqlrgeaeqlkqldaracadvtlaelvsglevgvomrttrtlrghlakia 60
 QY 61 MHMATDSKLLVASASDQGLIWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 61 mhmatdskllvasasdgqgkllwdsytnkvhaiplrswmtcayapsgnfvacggldnm 120
 QY 121 CSITNLKSRGVNWKVSRSLAHGTYLSCCRFLDDNNITVSSDPTCALMDIETGQKTFV 180
 121 csitnlksregvnwksrslahgtylscrrfldnnitvssdptcalmdietgqktvf 180
 QY 181 VGHGTGCMKSLAVSPDFNLFTISGACDASAKLMDVREGTCRQFTGHSDDINACFPNGEA 240
 181 vghgtgcmkslavspdfnlftisgacdasaaklmdvregtcrtqftghsddinaicfpngea 240
 Db 181 vghgtgcmkslavspdfnlftisgacdasaaklmdvregtcrtqftghsddinaicfpngea 240
 QY 241 ICTGSDDASCRFLRADQELICFHSHEITGITSVAFSLGRLLFAGYDFFNCVWDSM 300
 241 ictgsddascriflradqelicfshesitgitsvafslgrllfagyddfncvwdsm 300
 QY 301 KSERVGIISGHDNRVSCIGYADGMAVATGSDSEFLKINW 340
 301 kservgilsghdnrvscigvadgmavatsgswsflikwn 340
 Db 301 kservgilsghdnrvscigvadgmavatsgswsflikwn 340

RESULT 2

AA15169 standard; Protein: 340 AA.

AA15169;

12-DEC-2000 (first entry)

Human Taste Cell specific G-protein beta 3 subunit.

Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbetas3;
 taste transduction pathway; pharmaceutical; food industry.

Homo sapiens.

WO200045179-A2.

03-AUG-2000.

26-JAN-2000; 2000WO-US02218.

27-JAN-1999; 99US-0117404.

(REGC) UNIV CALIFORNIA.

Zuker CS, Adler JE, Lindemeier J;

WPI; 2000-49361/44.

N-PSDB; AAA74591.

XX Identifying a compound that modulates sensory signalling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PS polypeptide.

Claim 1; Page 63; 68pp; English.

The present sequence is human G-protein beta 3 subunit. G-protein beta 3
 CC is expressed specifically in taste cells, hence this sequence is referred
 CC to as "Taste Cell specific G-protein beta 3 subunit (TC-Gbetas3)". TC-Gbetas3
 CC is involved in the taste transduction pathway. TC-Gbetas3 may be used for
 CC identifying taste modulating compounds which can be used in
 CC pharmaceutical and food industries to customise taste.

Sequence 340 AA;

Query Match 100.0%; Score 1809; DB 21; Length 340;
 Best Local Similarity 100.0%; Pred. No. 5.3e-171;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMOLROEAEOLKQIADARACADVTTLAEVSGLEVGVOMRTTRTLRGLAKIYA 60
 1 mgemeqlrgeaeqlkqldaracadvtlaelvsglevgvomrttrtlrghlakia 60
 Db 61 MHMATDSKLLVASASDQGLIWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 61 mhmatdskllvasasdgqgkllwdsytnkvhaiplrswmtcayapsgnfvacggldnm 120
 QY 121 CSITNLKSRGVNWKVSRSLAHGTYLSCCRFLDDNNITVSSDPTCALMDIETGQKTFV 180
 121 csitnlksregvnwksrslahgtylscrrfldnnitvssdptcalmdietgqktvf 180
 QY 181 VGHGTGCMKSLAVSPDFNLFTISGACDASAKLMDVREGTCRQFTGHSDDINACFPNGEA 240
 181 vghgtgcmkslavspdfnlftisgacdasaaklmdvregtcrtqftghsddinaicfpngea 240
 Db 181 vghgtgcmkslavspdfnlftisgacdasaaklmdvregtcrtqftghsddinaicfpngea 240
 QY 241 ICTGSDDASCRFLRADQELICFHSHEITGITSVAFSLGRLLFAGYDFFNCVWDSM 300
 241 ictgsddascriflradqelicfshesitgitsvafslgrllfagyddfncvwdsm 300
 QY 301 KSERVGIISGHDNRVSCIGYADGMAVATGSDSEFLKINW 340
 301 kservgilsghdnrvscigvadgmavatsgswsflikwn 340
 Db 301 kservgilsghdnrvscigvadgmavatsgswsflikwn 340

RESULT 3

AA167865 standard; Protein: 340 AA.

AA167865;

25-APR-2000 (first entry)

Human Hgbb3 G-protein beta3 subunit amino acid sequence.

Ste20p/PAK; G-protein-coupled receptor signal transduction; human; Hgbb3;
 Ste4p/Gbeta interaction domain; p21-activated protein kinase;
 G-protein coupled receptor signal transduction;

Homo sapiens.

CA2219958-A1.

07-JUL-1999.

07-JAN-1998; 98CA-2219958.

07-JAN-1998; 98CA-2219958.

(LEBE/) LEBERER E.

(LEBU/) LEBOW T.


```

Db      301 kservylsgphdnrvscigtadgmavatsgwsdfikwn 340
|||||
RESULT 6
ID      AAB15175
XX      AAB15175 standard; Protein; 340 AA.
AC      AAB15175;
DT      12-DEC-2000 (first entry)
DE      Mutant human Taste Cell specific G-protein beta 3 subunit variant #3.
KW      Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
KW      taste transduction pathway; pharmaceutical; food industry; mutation;
KV      mutant.
XX      Homo sapiens.
OS      Synthetic.
XX      Key Location/Qualifiers
FH      Misc-difference 301
FT      /note= "Wild-type lys substituted by Arg"
PN      WO200045179-A2.
XX      03-AUG-2000.
PD      26-JAN-2000; 2000WO-US02218.
PE      27-JAN-1999; 99US-0117404.
PR      XX
PA      (REGC ) UNIV CALIFORNIA.
XX      PI
PI      Zuker CS, Adler JE, Lindemeier J;
DR      MPI; 2000-499361/44.
XX      Identifying a compound that modulates sensory signaling in sensory
PT      cells for use in pharmaceutical and food industries comprises
PT      contacting the compound with a sensory cell specific G-protein beta
PT      polypeptide -
XX      Dicalcium

```

CC	The present sequence is a mutant human G-protein beta 3 subunit.
CC	G-protein beta 3 is expressed specifically in taste cells, hence this
CC	sequence is referred to as taste cell specific G-protein beta 3 subunit
CC	(TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
CC	TC-Gbeta3 may be used in identifying taste modulating compounds which
CC	can be used in pharmaceutical and food industries to customise taste.
CC	Note: The present sequence is not shown in the specification but is
CC	derived from the human wild-type TC-Gbeta3 sequence given on page 63
XX	(see AAB15169) and information given on page 8 of the disclosure.
SQ	Sequence 340 AA:
Query Match	99.8%; Score 1806; DB 21; Length 340;
Best Local Similarity	99.7%; Pred. No. 1..1e-170;
Matches 339; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
OY	1 MGEMEDLRDAEQLKROIDARKACADVTLAELVSGLEVGVGRVQMRRRLRGLAKIYA 60
Db	1 mgemeglrgaeagllkqdadatcacadvclaelvsglevygvgrvtirrlrghlakia 60
OY	61 MHNAATSKLLVSAHSDGKLIVDSTYTNKKVAIPLRSSWMTCAVAPSGNFVAGCGLDNN 120
Db	61 mhwaatsklilveasdgdklilwdsyttnkvhaplrsswtmtcaavpsgnfvaacgldnn 120
OY	121 CSTYNLKSEGWVKYSRELSAHTGYLSCRFLEDDNNTVISSGGDTTCLMDLIETGOOKTVF 180

Db 121 cslynlksregnvkvsrelsahlylscrrfldnnlytssgdtlcalwldetgqktvf 180
 QY 181 VGHGDCMSLAVSPDFNLFISGACDASAKLMDVREGTCROTFTGHESDINATCFPPNGEA 240
 Db 181 vghgdcmslavspdfnlfisgacdasaklmdvregtcrotftghesdinaicffpnga 240
 QY 241 ICTGSDASCRFLRADOELICFHSHEIICGITSVAFSLSGRLLFAGYDPCNWNWDSM 300
 Db 241 ictgsdascrflraddelicfsheslicgitsvafslsgrlllfagyddfnncnwds 300
 QY 301 KSERVGLISGHDNRVSCIGVTADGMAVATGSDSFLKIMN 340
 Db 301 kservglisghdnrvscigvtadgmavatgswdsflkiwn 340
 RESULT 7
 ID AAB15170 standard; Protein: 340 AA.
 AC AAB15170;
 XX
 DT 12-DEC-2000 (first entry)
 DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #1.
 KW Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 KW mutant; mutant.
 OS Rattus sp.
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 8 /note= "Wild-type Lys substituted by Arg"
 PN WO200045179-A2.
 XX 03-AUG-2000.
 PD 26-JAN-2000; 2000WO-US02218.
 PF 27-JAN-1999; 99US-0117404.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX Zuker CS, Adler JE, Lindemeier J;
 DR WPI; 2000-499361/44.
 XX
 PT Identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -
 PS Disclosure; Page -: 68pp; English.
 XX
 CC The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
 CC beta 3 is expressed specifically in taste cells, hence this sequence is
 CC referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).
 CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
 CC be used for identifying taste modulating compounds which can be used in
 CC pharmaceutical and food industries to customise taste.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see
 CC AAB15168) and information given on page 8 of the disclosure.
 CC
 SQ Sequence 340 AA:

Query Match 97.6%; Score 1765; DB 21; Length 340;
 Best Local Similarity 96.8%; Pred. No. 1.2e-166;
 Matches 329; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEQLROEAQLKKOIAADARKACADVTLLAELVSGLEVGVQOMRTTRRLRGHLAKTYA 60
 Db 1 mgemeqlrgeeqkklkqdadarkacadtllaelysglevgvqomrttrrlirhlakiya 60
 QY 61 MHMATDSKLVASQDGLKIWDSYTTNKVAIPLRSSWWTCAVAPSGNFVACGIDNM 120
 Db 61 mhmatdsklvasaqdgklliwdtlytnkvaiplrsswmtcayapsgnfvacgiddm 120
 QY 121 CSYNAKSRBNVAVSRSLAHNGYLSCCRFLDNNIVTSSGDTTCLMNIENFGQKTVF 180
 Db 121 csynlksregnvkvsrelsahlylscrrfldnnlytssgdtlcalwldetgqktvf 180
 QY 181 VGHGDCMSLAVSPDFNLFISGACDASAKLMDVREGTCROTFTGHESDINATCFPPNGEA 240
 Db 181 vghgdcmslavspdfnlfisgacdasaklmdvregtcrotftghesdinaicffpnga 240
 QY 241 ICTGSDASCRFLRADOELICFHSHEIICGITSVAFSLSGRLLFAGYDPCNWNWDSM 300
 Db 241 ictgsdascrflraddelicfsheslicgitsvafslsgrlllfagyddfnncnwds 300
 QY 301 KSERVGLISGHDNRVSCIGVTADGMAVATGSDSFLKIMN 340
 Db 301 kservglisghdnrvscigvtadgmavatgswdsflkiwn 340
 RESULT 8
 ID AAB15168 standard; Protein: 340 AA.
 AC AAB15168;
 XX
 DT 12-DEC-2000 (first entry)
 DE Rat Taste Cell specific G-protein beta 3 subunit.
 KW Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry.
 OS Rattus sp.
 OS
 PN WO200045179-A2.
 XX 03-AUG-2000.
 PD 26-JAN-2000; 2000WO-US02218.
 PF 27-JAN-1999; 99US-0117404.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX Zuker CS, Adler JE, Lindemeier J;
 DR WPI; 2000-499361/44.
 DR N-PSDB; AAA74590.
 XX
 PT Identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -
 PS Claim 1; Page 62; 68pp; English.
 XX
 CC The present sequence is rat G-protein beta 3 subunit. G-protein beta 3 is
 CC expressed specifically in taste cells, hence this sequence is referred to
 CC as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is
 CC involved in the taste transduction pathway. TC-Gbeta3 may be used for
 CC identifying taste modulating compounds which can be used in
 CC pharmaceutical and food industries to customise taste.
 CC
 SQ Sequence 340 AA:

Query Match 97.4%; Score 1762; DB 21; Length 340;
 Best Local Similarity 96.5%; Pred. No. 2.4e-166;
 Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEOLROEAEOLKQIADARKACADVTLAELVSGLEVGVGMRTRRRLRGHLAKIYA 60
 DQ 1 mgemeqlkgeaeqlkqadarkacadtlaelvsglevgvgrvmtrrrlrghlakiya 60
 QY 61 MHMATDSEKLLVASASODGKLIWDSYTTNKVHAIPLRSSVWMTCAVAPSGNFVACGGLDM 120
 DQ 61 mhmatdskllvasasodgkllwtdytnkvhaiplrssvwmtecaypsngnfvacgglldm 120
 QY 121 CSTYNNKSRGKVKVSRRELSAHTGYISCCRFDDNNIYSSGDTTCALMDIETGQKTVF 180
 DQ 121 cstylnksrkvksrrelsahtgyisccrflddnniylssgdttcaldietgqktvf 180
 QY 181 VGHGDCMSLAVSPDFLFTSGACDASAKLMDVREGTCRQFTGHESDINMICFPNGEA 240
 DQ 181 vghgdcmslavspdfllftsgacdasaaklmdvregtcrcftghesdinalciffpnea 240
 QY 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFSLSGRLLFAGYDDFNQNVWDSM 300
 DQ 241 ictgsddascrlfdlradqelctayshesilcgtlsvafslsgrllfagyddfnncvwsd 300
 QY 301 KSERVGIISGHDNRVSCLGVTADGMAVATGSDSFLKIWN 340
 DQ 301 kservgiisghdnrvsclgvtadgmaavatgsdflkiwn 340

RESULT 9
 AAB15171 ID AAB15171 standard; Protein: 340 AA.
 AC AAB15171;
 DT 12-DEC-2000 (first entry)
 DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #2.
 KM Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KM taste transduction pathway; pharmaceutical; food industry; mutation;
 KM muteln; mutant.
 OS Rattus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 12 /note= "Wild-type Glu substituted by Asp"
 FT
 XX WO200045179-A2.
 XX
 XX PD 03-AUG-2000.
 XX
 XX PF 26-JAN-2000; 2000WO-US02218.
 XX
 XX PR 27-JAN-1999; 99US-0117404.
 XX
 XX PA (REGC) UNIV CALIFORNIA.
 XX
 XX PI Zuker CS, Adler JE, Lindemeyer J;
 XX
 XX DR WPI; 2000-499361/44.
 XX
 XX PT Identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -
 XX
 XX PS Disclosure; Page -: 68pp; English.
 XX
 CC The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
 CC beta 3 is expressed specifically in taste cells, hence this sequence is

CC referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).
 CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
 CC be used for identifying taste modulating compounds which can be used in
 CC pharmaceutical and food industries to customise taste.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the rat wild-type TC-Gbeta3 sequence given on page 62 (see
 CC AAB15168) and information given on page 8 of the disclosure.
 XX
 SO Sequence 340 AA;

Query Match 97.2%; Score 1759; DB 21; Length 340;
 Best Local Similarity 96.2%; Pred. No. 4.8e-166;
 Matches 327; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEOLROEAEOLKQIADARKACADVTLAELVSGLEVGVGMRTRRRLRGHLAKIYA 60
 DQ 1 mgemeqlkgeaeqlkqadarkacadtlaelvsglevgvgrvmtrrrlrghlakiya 60
 QY 61 MHMATDSEKLLVASASODGKLIWDSYTTNKVHAIPLRSSVWMTCAVAPSGNFVACGGLDM 120
 DQ 61 mhmatdskllvasasodgkllwtdytnkvhaiplrssvwmtecaypsngnfvacgglldm 120
 QY 121 CSTYNNKSRGKVKVSRRELSAHTGYISCCRFDDNNIYSSGDTTCALMDIETGQKTVF 180
 DQ 121 cstylnksrkvksrrelsahtgyisccrflddnniylssgdttcaldietgqktvf 180
 QY 181 VGHGDCMSLAVSPDFLFTSGACDASAKLMDVREGTCRQFTGHESDINMICFPNGEA 240
 DQ 181 vghgdcmslavspdfllftsgacdasaaklmdvregtcrcftghesdinalciffpnea 240
 QY 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFSLSGRLLFAGYDDFNQNVWDSM 300
 DQ 241 ictgsddascrlfdlradqelctayshesilcgtlsvafslsgrllfagyddfnncvwsd 300
 QY 301 KSERVGIISGHDNRVSCLGVTADGMAVATGSDSFLKIWN 340
 DQ 301 kservgiisghdnrvsclgvtadgmaavatgsdflkiwn 340

RESULT 10
 AAB15172 ID AAB15172 standard; Protein: 340 AA.
 AC AAB15172;
 DT 12-DEC-2000 (first entry)
 DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #3.
 KM Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KM taste transduction pathway; pharmaceutical; food industry; mutation;
 KM muteln; mutant.
 OS Rattus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 191 /note= "Wild-type Ala substituted by Gly"
 FT
 XX WO200045179-A2.
 XX
 XX PD 03-AUG-2000.
 XX
 XX PF 26-JAN-2000; 2000WO-US02218.
 XX
 XX PR 27-JAN-1999; 99US-0117404.
 XX
 XX PA (REGC) UNIV CALIFORNIA.
 XX
 XX PI Zuker CS, Adler JE, Lindemeyer J;
 XX
 XX

DR WPI: 2000-499361/44.
 XX Identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -
 XX
 PS Disclosure; Page -: 68pp; English.
 XX
 CC The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
 CC beta 3 is expressed specifically in taste cells, hence this sequence is
 CC referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).
 CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
 CC be used for identifying taste modulating compounds which can be used in
 CC pharmaceutical and food industries to customize taste.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see
 CC AAB15168) and information on page 8 of the disclosure.
 XX
 SQ Sequence 340 AA;

Query Match 97.2%; Score 1758; DB 21; Length 340;
 Best Local Similarity 96.2%; Pred. No. 6.1e-166;
 Matches 327; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MGEMEDLRQAEOLKQADARACADVTLAELVSGLEVGVGMRTFRLRGHLAKIYA 60
 DB 1 mgemeqlkgeaeqlkqadardacacdltaelvslevvgvgrmttrtlrghlakkia 60
 QY 61 MHVATSKLIVASADGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
 DB 61 mhvatasklivasdgklliwdsyttknvhaiplrsswmtcavapsngnfvaacgglldm 120
 QY 121 CSYINLKSREGNVKVSRLSAHTGYLSCRFDDNNIVTSSGDTTCALMDIEGQOKTYF 180
 DB 121 csylnlksregnvksrslsahthgytscrrfdnnivtssgdttcaldieggoktyf 180
 QY 181 VGHGTGCMSLAVSPDFNLFTISGACDASAKLMDVREGTCRQFTTGHESDINACFFPNGEA 240
 DB 181 vghgtgcmslavspdfnlfisgacdasaklmdvregtcrcrfttgghesdinaicffpnga 240
 QY 241 ICTGSDASCRLFDLRADDELICFSHESIIGTTSVAFSLGRLLFAGYDDPNCNVWDSM 300
 DB 241 ictgsdascrlfdlradeleicfshesitigttsvafslgrllfagyddpncnvwdsm 300
 QY 301 KSERVGIILSGHDNRVSCIGVTADGMAVATGSMDSFLKIMN 340
 DB 301 kservgiilsghdnrvscigvtadgmaavatgsmdsflkimn 340
 Kcervgvlsghdnrvscigvtadgmaavatgswdsflkimn 340

RESULT 11
 AAR85859
 ID AAR85859 standard; peptide; 340 AA.
 XX
 AC AAR85859;
 XX
 DT 13-SEP-1996 (first entry)
 XX
 DE WD-40 domain-contg. bovine G-beta-1 protein.
 XX
 KW WD40 repeat region; beta-transducin; protein-protein interaction; drug;
 KM intracellular signalling; protein kinase C; homology; motif; modulator;
 XX receptors of activated protein kinase; enzyme activity; isozyme; human.
 OS Bos taurus.
 XX
 PN W09521252-A2.
 XX
 PD 10-AUG-1995.
 XX
 PF 31-JAN-1995; 95WO-US01210.
 XX

PR 01-FEB-1994; 94US-0190802.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Mochly-Rosen D, Ron D;
 XX
 DR WPI: 1995-283772/37.
 XX
 PT New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
 PT activity of a protein, eg. protein kinase C, which interacts with a
 PT protein contg. a WD-40 region.
 XX
 PS Example 5; Page 102-103; 351pp; English.
 XX

CC Proteins AAR85851-92 are protein which contain at least one WD-40 (also
 CC called beta-transducin homologous) amino acid repeat motifs. The WD-40
 CC regions are involved in protein-protein interactions between proteins
 CC involved in intracellular signalling. An example of such an interaction
 CC is between protein kinase C and receptors of activated protein kinase
 CC (RACK), esp. RACK-1 (AAR85850). Proteins AAR85851-82 were isolated based
 CC on homology with beta-transducin, whereas proteins AAR85882-92 were
 CC isolated based on homology with the WD-40 consensus sequence (AAR85893).
 CC The proteins were used to construct the peptides AAR84928-R85063 and
 CC AAR85786-R85842. The peptides can be used to identify target proteins
 CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
 CC proteins involved in protein-protein interaction and to screen for drugs
 CC that will affect protein-protein interaction involving WD-40 domains.
 XX
 SQ Sequence 340 AA;

Query Match 87.2%; Score 1578; DB 16; Length 340;
 Best Local Similarity 83.2%; Pred. No. 4.2e-148;
 Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;
 QY 1 MGEMEDLRQAEOLKQADARACADVTLAELVSGLEVGVGMRTFRLRGHLAKIYA 60
 DB 1 mseldqlrgeaeqlkngldardacacdelstgtnldpygrlmttrtlrghlakkia 60
 QY 61 MHVATSKLIVASADGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
 DB 61 mhvatasklivasdgklliwdsyttknvhaiplrsswmtcavapsngnfvaacgglldm 120
 QY 121 CSYINLKSREGNVKVSRLSAHTGYLSCRFDDNNIVTSSGDTTCALMDIEGQOKTYF 180
 DB 121 csylnlksregnvksrslsahthgytscrrfdnnivtssgdttcaldieggoktyf 180
 QY 181 VGHGTGCMSLAVSPDFNLFTISGACDASAKLMDVREGTCRQFTTGHESDINACFFPNGEA 240
 DB 181 vghgtgcmslavspdfnlfisgacdasaklmdvregtcrcrfttgghesdinaicffpnga 240
 QY 241 ICTGSDASCRLFDLRADDELICFSHESIIGTTSVAFSLGRLLFAGYDDPNCNVWDSM 300
 DB 241 ictgsdascrlfdlradeleicfshesitigttsvafslgrllfagyddpncnvwdsm 300
 QY 301 KSERVGIILSGHDNRVSCIGVTADGMAVATGSMDSFLKIMN 340
 DB 301 kservgiilsghdnrvscigvtadgmaavatgsmdsflkimn 340
 Kdravgvlgahdnrvscigvtdgmaavatgswdsflkimn 340

RESULT 12
 AAY67863
 ID AAY67863 standard; protein; 340 AA.
 XX
 AC AAY67863;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human Hgb1 G-protein beta1 subunit amino acid sequence.
 XX
 KW Ste20p/PAK: G-protein-coupled receptor signal transduction; human; Hgb1;
 KM Ste4p/Gbeta interaction domain; p21-activated protein kinase;
 KW G-protein coupled receptor signal transduction;

XX OS Homo sapiens.
 XX PN CA2219958-A1.
 XX PD 07-JUL-1999.
 XX PF 07-JAN-1998; 98CA-2219958.
 XX PR 07-JAN-1998; 98CA-2219958.
 XX PA (LEBERER) LEBERER E.
 XX PA (LEWU) LEWU T.
 XX PA (THOM) THOMAS D Y.
 XX PA (WHIT) WHITEWAY M.
 XX PI Leberer E, Leeuw T, Thomas DY, Whiteway M;
 XX DR WPI: 2000-137553/13.
 XX PT Interacting polypeptides involved in G-protein-coupled receptor signal
 XX PT transduction -
 XX PS Claim 3: Fig 6: 91pp: English.

CC This sequence represents the beta subunit of a human G-protein. The
 CC invention relates to the G-protein beta subunit interaction domain of the
 CC Ste20p/PAK family of protein kinases. The Ste20p/PAK family of protein
 CC kinases are p21-activated protein kinases (PAK), and they are involved in
 CC many varied cellular processes ranging from morphogenesis and stress
 CC response, to apoptosis. Interacting polypeptides Steap/Gbeta and
 CC Ste20p/PAK are useful for designing in vitro and in vivo experimental
 CC models which enable the screening of large collections of synthetic,
 CC semi-synthetic, or natural compounds for therapeutic use in Steap/Gbeta
 CC and Ste20p/PAK dependent diseases.

XX Sequence 340 AA:
 SO
 Query Match 87.2%; Score 1578; DB 21; Length 340;
 Best Local Similarity 83.2%; Pred. No. 4,2e-148;
 Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGMEQLROEADOLKQIADARKACADVTLAELVSGLEVGRVQRTTRTLRGLAKIYA 60
 DB 1 mselqqlrgeaeqlkqqladarkacadaelsgltmldpvgtrgmtrtlrghlakiya 60

QY 61 MHNATDSKLLVSAASODGKLIYWDSTYTNKVHAIPLRSSWVMCAVAPSGNFVACGLDNN 120
 DB 61 mhngtdsrllvsaasqgkllvwdstynkvhaiprlsswvmcavapsngnyvacgglldnn 120

QY 121 CSITNLSKREGNKKVSAASODGKLIYWDSTYTNKVHAIPLRSSWVMCAVAPSGNFVACGLDNN 180
 DB 121 csitnlskregnkvksrelsahtgylsccrfldnnvssgdtlcalmdietgooktve 180

QY 181 VGHFGDCMSLAVSPDENLIFSGACDASAKLMVREGTCROTFTGHESDINAICFPFNGEA 240
 DB 181 tghfgdcmslsvspdenlflfsgacdasaklmvregtcrotftghesdinaicffpnga 240

QY 241 ICGSDASCRFLFDRADDELICFHSHEITIGTVAFLSGRLIFAGYDDFCNVWDSM 300
 DB 241 fatgsdascrlfdraddelicfshesitigtsvafslsgrllfagyddfcncvwdsm 300

QY 301 KSERVGLSGHNDNRVSCLGVTADGMAVATGSMDSFLKIWN 340
 DB 301 kdragvlagndnrsvsclyvldgmvavagswdsflkiwn 340

RESULT 13
 ID AAM59364 standard; Protein: 299 AA.
 XX AAM59364;
 AC

XX DT 10-SEP-1998 (first entry)
 XX DE Human G-protein beta-3 subunit protein.
 XX KW G protein; beta-3 subunit; human; hypertension; immunodeficient; stroke;
 XX KW treatment; cardiovascular disease; metabolic disorder; tumour metastasis;
 XX KW coronary heart disease; post-angioplastic re-stenosis; diabetes;
 XX KW nephropathy; polynuropathy; retinopathy.
 XX OS Homo sapiens.
 XX PN WO9811212-A1.
 XX PD 19-MAR-1998.
 XX PF 29-AUG-1997; 97WO-EP04709.
 XX PR 13-SEP-1996; 96DE-1037518.
 XX PA (SIFERT) SIFERT W.
 XX P1 Sifert W;
 XX DR WPI: 1998-271665/24.
 XX DR N-PSDB: AAV34857.
 XX PT Variant of human G protein beta-3 sub-unit - associated with
 XX PT hypertension
 XX PS Claim 2: Page 12-13: 34pp: German.

CC This sequence represents a human G-protein beta-3 subunit consisting
 CC of up to six WD repeat motifs (as found in hypertensive subjects, rather
 CC than the seven WD repeat motifs found in normotensive subjects). The
 CC nucleic acid sequence encoding this protein can be expressed in a host
 CC organism to produce the protein, preferably where the host organism is an
 CC immunodeficient person, especially an HIV-positive person. This sequence
 CC can be used to prepare a medicament for treating diseases associated with
 CC G protein mis-control e.g. cardiovascular disease, metabolic disorders or
 CC immunological diseases, hypertension, coronary heart disease, stroke,
 CC post-angioplastic re-stenosis, diabetic complications (e.g. nephropathy,
 CC polynuropathy or retinopathy) or tumour metastasis.

XX Sequence 299 AA:
 SO
 Query Match 86.2%; Score 1558.5; DB 19; Length 299;
 Best Local Similarity 87.9%; Pred. No. 3e-146;
 Matches 299; Conservative 0; Mismatches 0; Indels 41; Gaps 1;

QY 1 MGMEQLROEADOLKQIADARKACADVTLAELVSGLEVGRVQRTTRTLRGLAKIYA 60
 DB 1 mgemeqlrgeaeqlkqqladarkacadvlaelvsglevgrvqmrtrtlrghlakiya 60

QY 61 MHNATDSKLLVSAASODGKLIYWDSTYTNKVHAIPLRSSWVMCAVAPSGNFVACGLDNN 120
 DB 61 mhwatdsklvsaasqgkllvwdstynkvhaiprlsswvmcavapsngnfvacgglldnn 120

QY 121 CSITNLSKREGNKKVSAASODGKLIYWDSTYTNKVHAIPLRSSWVMCAVAPSGNFVACGLDNN 180
 DB 121 csitnlskregnkvksrelsahtgylsccrfldnnvssgdtlcalmdietgooktve 180

QY 181 VGHFGDCMSLAVSPDENLIFSGACDASAKLMVREGTCROTFTGHESDINAICFPFNGEA 240
 DB 181 vghfgdcmslsvspdenlflfsgacdasaklmvregtcrotftghesdinaicffpnga 240

QY 241 ICGSDASCRFLFDRADDELICFHSHEITIGTVAFLSGRLIFAGYDDFCNVWDSM 300
 DB 241 icggsdascrlfdraddelicfshesitigtsvafslsgrllfagyddfcncvwdsm 300

QY 301 KSERVGLSGHNDNRVSCLGVTADGMAVATGSMDSFLKIWN 340
 DB 301 kservgllsgndnrsvsclyvldgmvavagswdsflkiwn 340

DB 260 kservgilsgdhnrsvclgvtadgmavatsgwsdfiklwn 299

RESULT 14

AAW90939 ID AAW90939 standard; Protein; 297 AA.

AAW90939; XX

14-JUL-2000 (first entry)

Human G-protein beta3 subunit Gbetas3-2 protein.

Human: G-protein; beta3 subunit; anti-diabetic; cardiact; osteoporotic; obesity; hypercholesterolemia; coronary heart disease; osteoporosis; myocardial infarct; atherosclerosis; neurodegenerative; hormone therapy; cerebrovascular disease; Alzheimer's disease.

OS Homo sapiens.

W0200015785-A2.

23-MAR-2000.

06-SEP-1999; 99WO-EP06534.

10-SEP-1998; 98DE-1041299.

05-FEB-1999; 99DE-1004825.

18-MAR-1999; 99DE-1012049.

29-MAR-1999; 99DE-1014229.

30-APR-1999; 99DE-1019889.

21-MAY-1999; 99DE-1023539.

(SIFP/) SIFFERT W.

SIffert W;

WPI: 2000-271425/23.

N-PSDB; AAA11700.

A novel gene for a variant Gb3-subunit of human G-protein

useful for determining risk of G-protein dysfunction associated disease

Claim 27; Page 77-78; 78pp; German.

This invention describes novel Gbetas3-subunits of the human G-protein. The products of the invention have anti-diabetic, cardiact, osteoporotic and neuroprotective activity. Polymorphisms identified in the Gbetas3 subunit coding sequence, especially C825T and/or C1429T, can be used to identify a risk of a disease or illness associated with G-proteins dysfunction. Such diseases include diabetes mellitus type 2, excess weight and obesity, hypercholesterolemia, coronary heart disease, myocardial infarct, sudden heart death, osteoporosis, atherosclerosis, neurodegenerative or cerebrovascular diseases, in particular Alzheimer's disease, an illness based on an increased reaction of the immune system and/or a non-erectile dysfunction. The polymorphisms can also be used to predict risk in women of cardiovascular disease. In particular high blood pressure or coronary heart disease and to direct hormone therapy to reduce risk of cardiovascular risk. The sequence information can also be used to determine if there is an increased risk for HIV-positive homozygote patients of developing AIDS. An alteration in the Gbetas3-subunit, as above, can be used to identify a person with an increased CO₂- or rather a hypoxic tolerance. The polymorphism can also be used to determine the responsiveness of a patient to in vivo hormones, transmitters (also neurotransmitters) or drugs, that activate G-protein heterotimers, which influence stimulation of G-protein subunits Gbetas3 and Gbetas3 and/or Galphas. The sequence data and methods can be used to determine specific therapies and doses for treatment of the above diseases, especially acute myocardial infarct with or without heart rhythm disturbance and transplant rejection. In particular, it can be used to predict the activity of a dose of erythropoietin on blood

CC formation and/or predicting the formation of hypertension under this
CC therapy. The method can be used to predict the danger of hypertension when
CC using immunosuppressive therapy, in particular cyclosporin. It is also
CC possible to predict the responsiveness of a patient in vivo to a
CC substance with prostaglandin E1 activity. Complementary sequences to the
CC Gbetas3 subunit nucleic acid sequences can be used for antisense
CC medicaments for therapy or prevention of disease. The Gbetas3 subunit of
CC human G-protein can be used in a recombinant system or after transfection
CC into a relevant cell to identify chemicals which function as inhibitors
CC of Gbetas3. Nucleic acid sequences encoding Gbetas3 can be used to
CC prepare transgenic animals and to produce medicaments for treatment of
CC misdirected G-protein associated diseases. The Gbetas3 protein can also
CC be used to produce specific antibodies. This sequence represents the
CC human G-protein Gbetas3 subunit described in the method of the invention.
XX
SQ Sequence 297 AA;

Query Match
Best Local Similarity 85.6%; Score 1548.5; DR 21; Length 297;
Matches 297; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MGEMEDLROEAEQKROIDARKACADVTLAELVSGLEWVGWQMTFRRLRGHLAKIYA 60
DB 1 mgemeqlrgeaeqlkqgldarkacadvlaelvgslvgyvqmttrtlrghlaktiya 60
QY 61 MHVATDSKILLVSAQDGKLIWDSYTNKVAIPLRSSWVTCAYAPSGNFVACGGLDNM 120
DB 61 mhvatdskillvasagdgkllwdsytnkvahiplrswvmtcayapsngfvacggladm 120
QY 121 CSTIYNLKSREGNWKVRSRLSAHTGYLSCRFDDNNINWSSGDTTCALMDFTGQOKTVE 180
DB 121 cs1ynlksregnvkrsrlsahthgyiscrfddnnilvssgdtccalmdftgqktvf 180
QY 181 VGHGTGDKSLAVSPDPNLFISGACDASAKLMVDREGTCROTFTGHESINMICEFPNGEA 240
DB 181 vghgtgdkmslavsdpdnlflisgacdasaklwdvregtcrotftghesinmicef----- 234
QY 241 ICTGSDASCRFLFDLRADQELICFSHESIICGITSVAISLSGRLLFAGYDDFNCCNWDNM 300
DB 241 ictgsdascrflfdlradqelicfshesiiicgitsvasislsgrllfagyddfnccnwdnm 300
QY 301 KSERVGIISGHDNRVSCIGVTADGMNAVATGWSDFLKIWN 340
DB 258 kservgilsgdhnrsvclgvtadgmavatsgwsdfiklwn 297

RESULT 15

AAW85863 ID AAW85863 standard; peptide; 340 AA.

AAW85863; XX

13-SEP-1996 (first entry)

WD-40 domain-contg. human G-beta-2 protein.

WD40 repeat region; beta-transducin; protein-protein interaction; drug; intracellular signalling; protein kinase C; homology; motif; modulator; receptors of activated protein kinase; enzyme activity; isozyme; human.

Homo sapiens.

W09521252-A2.

10-AUG-1995.

31-JAN-1995; 95WO-US01210.

01-FEB-1994; 94US-0190802.

(STRD) UNIV LEIAND STANFORD JUNIOR.

Fri Sep 28 10:45:11 2001

us-09-492-029-5.rag

PI Mochly-Rosen D, Ron D;
 XX WPI: 1995-283772/37.

DR New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
 PT activity of a protein, eg. protein kinase C, which interacts with a
 PT protein contg. a WD-40 region.

XX
 PS Example 5; Page 109-110; 351pp; English.

XX Proteins AAR85851-92 are protein which contain at least one WD-40 (also
 CC called beta-transducing homologous) amino acid repeat motifs. The WD-40
 CC regions are involved in protein-protein interactions between proteins
 CC involved in intracellular signalling. An example of such an interaction
 CC is between protein kinase C and receptors of activated protein kinase
 CC (RACK), esp. RACK-1 (AAR85850). Proteins AAR85851-92 were isolated based
 CC on homology with beta-transducin, whereas proteins AAR85882-92 were
 CC isolated based on homology with the WD-40 consensus sequence (AAR85893).
 CC The proteins were used to construct the peptides AAR84928-R85063 and
 CC AAR85786-R85842. The peptides can be used to identify target proteins
 CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
 CC proteins involved in protein-protein interaction and to screen for drugs
 CC that will affect protein-protein interaction involving WD-40 domains.

XX Sequence 340 AA:

Query Match 84.5%; Score 1528; DB 16; Length 340;
 Best Local Similarity 80.9%; Pred. No. 3.8e-143;
 Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGEMLQLEAEQOLKQIADAKKACADVTAEVSGLEAVGRVOMTRRTLRGLAKIYA 60
 DB 1 mselqelrgeaelrnlrdarkacgdstltqtaqldpvgitqmrtrllrghlakiya 60
 QY 61 MHRATDSKILVASODGKLIWDSYTTNKVHAIPLRSSWMTCAIAPSGNFVACGGIDNM 120
 DB 61 mhwtldsrllvasasgqgkllwdsytnkvhailrswmtcayapsnlfvaccgldni 120
 QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNITVSSGDTTCALMDIETGQOKYVF 180
 DB 121 cslyslktrregnvrvarelpghnlgyscerfiddnqitssgdtcalwdietgqktyvf 180
 QY 181 VGHFGDMSLAVSPDFNLFIISGACDASAKLMDVREGTCROTFTGHESDINACFFPNGEA 240
 DB 181 aghsgdmslaspdgtrltfvsagcdasiklwdvrdsmcrtqftghesdinavalfpnyga 240
 QY 241 ICTGSDASCRFLPDADQELICFHSHTICGITSVAEFLSGRLFAGYDDPNCNWDSM 300
 DB 241 ftgsgddatcrlfdradqelimsnllcgltsvafarsgrlllagyddfnchlwam 300
 QY 301 KSERVGIISGHDNRVSCIGVTADGMAVATGSMDSFLKIWN 340
 DB 301 kgdragvlaghnrvsclygtcdgmavaltgswdsflkiwn 340

Search completed: September 28, 2001, 10:29:22
 Job time: 72 sec

Fri Sep 28 10:45:11 2001

us-09-492-029-5.rai

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:28:39 ; Search time 20.71 Seconds
(without alignments)
338.036 Million cell updates/sec

Title: US-09-492-029-5
1809
Perfect score: 1 MGEMEQLEQAEQLEKQKQAD.....TADGMVAATGSMDFLKTNN 340
Sequence: 1

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTCUG.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1809	100.0	340	US-09-180-783-2
2	1578	87.2	340	US-08-190-802A-38
3	1558.5	86.2	299	US-09-147-826B-2
4	1528	84.5	340	US-08-190-802A-42
5	1463	80.9	341	US-08-190-802A-45
6	1459	80.7	340	US-08-190-802A-40
7	1421	78.6	336	US-08-190-802A-39
8	949.5	52.5	395	US-09-032-372-1
9	650	35.9	423	US-08-190-802A-61
10	305.5	16.9	317	US-08-190-802A-27
11	305.5	16.9	317	US-08-190-802A-41
12	305.5	16.9	317	US-08-190-802A-47
13	296	16.4	704	US-08-190-802A-62
14	296	16.4	704	US-08-188-582-5
15	296	16.4	704	US-08-646-715-5
16	296	16.4	704	US-08-308-818-3
17	287	15.9	587	US-08-899-578-2
18	274	15.1	704	US-08-188-582-18
19	274	15.1	704	US-08-646-715-18
20	271.5	15.0	439	US-08-190-802A-65
21	265	14.6	318	US-08-190-802A-33
22	257.5	14.2	514	US-08-190-802A-66
23	251	13.9	798	US-08-190-802A-64
24	251	13.9	798	US-08-190-802A-68
25	251	13.9	798	US-08-308-818-2
26	247	13.7	713	US-08-190-802A-63
27	242	13.4	375	US-09-063-743-1

28	241.5	13.3	343	US-09-063-743-5	Sequence 5, Appl
29	239	13.2	305	US-08-965-600-1	Sequence 1, Appl
30	237	13.1	409	US-08-283-917-3	Sequence 3, Appl
31	237	13.1	409	US-08-961-716-3	Sequence 9, Appl
32	237	13.1	410	US-08-283-917-9	Sequence 9, Appl
33	237	13.1	410	US-08-961-716-9	Sequence 9, Appl
34	231.5	12.8	906	US-08-190-802A-31	Sequence 31, Appl
35	227.5	12.6	409	US-08-190-802A-51	Sequence 51, Appl
36	212.5	11.7	2627	US-08-751-189-3	Sequence 3, Appl
37	212.5	11.7	2627	US-09-060-836-3	Sequence 3, Appl
38	212.5	11.7	2627	US-09-184-445-3	Sequence 30, Appl
39	210	11.6	517	US-08-190-802A-30	Sequence 4, Appl
40	209	11.6	2629	US-08-751-189-4	Sequence 4, Appl
41	209	11.6	2629	US-09-060-836-4	Sequence 4, Appl
42	203.5	11.6	2629	US-09-184-445-4	Sequence 4, Appl
43	203.5	11.2	587	US-08-883-534-6	Sequence 6, Appl
44	203.5	11.2	587	US-09-204-764-6	Sequence 6, Appl
45	197.5	10.9	376	US-08-883-534-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1	US-09-180-783-2	US-09180783
Sequence 2, Application	US-09180783	
Patent No. 6242181		
GENERAL INFORMATION:		
APPLICANT: Sifert, Winfried		
TITLE OF INVENTION: THE USE OF A GENETIC MODIFICATION IN THE GENE FOR HUMAN		
FILE REFERENCE: 1135-2		
CURRENT APPLICATION NUMBER: US/09/180,783		
CURRENT FILING DATE: 1999-03-17		
PRIOR APPLICATION NUMBER: PCT/EP97/02250		
PRIOR FILING DATE: 1997-05-02		
PRIOR APPLICATION NUMBER: DE 19619362.1		
PRIOR FILING DATE: 1996-05-14		
NUMBER OF SEQ ID NOS: 4		
SOFTWARE: Patent Ver. 2.1		
SEQ ID NO 2		
LENGTH: 340		
TYPE: PRT		
ORGANISM: Homo sapiens		
US-09-180-783-2		
Query Match	Score 1809; DB 4; Length 340;	
Best Local Similarity	100.0%; Pred. No. 1.4e-171;	
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 1 MGEMEQLEQAEQLEKQKQADVTTLAEVSGLEVGVQMTKRTTLGHLAKTYA 60		
QY 1 MGEMEQLEQAEQLEKQKQADVTTLAEVSGLEVGVQMTKRTTLGHLAKTYA 60		
QY 61 MHVATDLSKLVASODGKLIYDSTTTKVAHPIRBSWVTCAYAPSGNFVACGIDNN 120		
QY 61 MHVATDLSKLVASODGKLIYDSTTTKVAHPIRBSWVTCAYAPSGNFVACGIDNN 120		
QY 61 MHVATDLSKLVASODGKLIYDSTTTKVAHPIRBSWVTCAYAPSGNFVACGIDNN 120		
QY 121 CSYINLKSRGNKYSRELSAHTGYLSCRFDDNNITVSSGDTTCALMDIETGQOKYVF 180		
QY 121 CSYINLKSRGNKYSRELSAHTGYLSCRFDDNNITVSSGDTTCALMDIETGQOKYVF 180		
QY 121 CSYINLKSRGNKYSRELSAHTGYLSCRFDDNNITVSSGDTTCALMDIETGQOKYVF 180		
QY 181 VGHGDCMSLAVSPDFNLISGACDASAKIMDYRGTCROFTGHESDINACFPNGEA 240		
QY 181 VGHGDCMSLAVSPDFNLISGACDASAKIMDYRGTCROFTGHESDINACFPNGEA 240		
QY 241 ICTGSDASCRFLPLRADDELICFHSHEITIGTTSVAVSLGRLLFAGYDPCNWDMSM 300		
QY 241 ICTGSDASCRFLPLRADDELICFHSHEITIGTTSVAVSLGRLLFAGYDPCNWDMSM 300		
QY 301 KSERVGIISGHDNVSCLGYTADGMAVATGSMDFLKTNN 340		

Db 301 KSERVILSGHDNRVSCLGVTADGMAVATGSMDSFLKINW 340

RESULT 2

US-08-190-802A-38
Sequence 38, Application US/08190802A
Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G-Beta 1 bovine, Fig. 21
US-08-190-802A-38

Query Match

Best Local Similarity 87.2%; Score 1578; DB 1; Length 340;
Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGEEOLOROEAEDLKQIADARRACADVTLAELVSGLEVGVGMOMRTTRTGRHLAKIYA 60
Db 1 MSELDOLOROEAEDLKQIADARRACADVTLAELVSGLEVGVGMOMRTTRTGRHLAKIYA 60
QY 61 MHWATDSKLVASQDGKLIWDSYTNKVAHPIPLRSSWMTCAVAPSGNVAACGGIDNM 120
Db 61 MHWATDSKLVASQDGKLIWDSYTNKVAHPIPLRSSWMTCAVAPSGNVAACGGIDNM 120
QY 121 CSTYLNKSRGNNKYSRELSTAGTGLSCRFDDNNITVSSGDTTCALMDIEGQOKTVF 180
Db 121 CSTYLNKSRGNNKYSRELSTAGTGLSCRFDDNNITVSSGDTTCALMDIEGQOKTVF 180
QY 181 VGHGTGMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTFGHESDINAIICFPNGEA 240
Db 181 VGHGTGMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTFGHESDINAIICFPNGEA 240
QY 241 ICTGSDDASCRFLDRADELICFHSIIIGITVAFLSGRLPAGYDDPFCNVWDSM 300
Db 241 ICTGSDDASCRFLDRADELICFHSIIIGITVAFLSGRLPAGYDDPFCNVWDSM 300
QY 301 KSERVILSGHDNRVSCLGVTADGMAVATGSMDSFLKINW 340
Db 301 KSERVILSGHDNRVSCLGVTADGMAVATGSMDSFLKINW 340

QY 301 KSERVILSGHDNRVSCLGVTADGMAVATGSMDSFLKINW 340
Db 301 KADRAVGLAGHDNRVSCLGVTADGMAVATGSMDSFLKINW 340

RESULT 3

US-09-147-826B-2
Sequence 2, Application US/09147826B
Patent No. 6251853

GENERAL INFORMATION:

APPLICANT: Siefert, Winfried
TITLE OF INVENTION: PTX-SENSITIVE G PROTEINS, THEIR PREPARATION AND USE
FILE REFERENCE: 1135-0003
CURRENT APPLICATION NUMBER: US/09/147,826B
CURRENT FILING DATE: 1999-03-15
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: PCT/EP97/04709
PRIOR FILING DATE: 1996-09-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-147-826B-2

Query Match 86.2%; Score 1558.5; DB 4; Length 299;
Best Local Similarity 87.9%; Pred. No. 8.3e-147;
Matches 299; Conservative 0; Mismatches 0; Indels 41; Gaps 1;

QY 1 MGEEOLOROEAEDLKQIADARRACADVTLAELVSGLEVGVGMOMRTTRTGRHLAKIYA 60
Db 1 MGEEOLOROEAEDLKQIADARRACADVTLAELVSGLEVGVGMOMRTTRTGRHLAKIYA 60
QY 61 MHWATDSKLVASQDGKLIWDSYTNKVAHPIPLRSSWMTCAVAPSGNVAACGGIDNM 120
Db 61 MHWATDSKLVASQDGKLIWDSYTNKVAHPIPLRSSWMTCAVAPSGNVAACGGIDNM 120
QY 121 CSTYLNKSRGNNKYSRELSTAGTGLSCRFDDNNITVSSGDTTCALMDIEGQOKTVF 180
Db 121 CSTYLNKSRGNNKYSRELSTAGTGLSCRFDDNNITVSSGDTTCALMDIEGQOKTVF 180
QY 181 VGHGTGMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTFGHESDINAIICFPNGEA 240
Db 181 VGHGTGMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTFGHESDINAIICFPNGEA 240
QY 241 ICTGSDDASCRFLDRADELICFHSIIIGITVAFLSGRLPAGYDDPFCNVWDSM 300
Db 241 ICTGSDDASCRFLDRADELICFHSIIIGITVAFLSGRLPAGYDDPFCNVWDSM 300
QY 301 KSERVILSGHDNRVSCLGVTADGMAVATGSMDSFLKINW 340
Db 260 KSERVILSGHDNRVSCLGVTADGMAVATGSMDSFLKINW 299

RESULT 4

US-08-190-802A-42
Sequence 42, Application US/08190802A
Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentln Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190, 802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 340 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: G-Beta 2 (Human), Fig. 25
 US-08-190-802A-42

Query Match 84.5%; Score 1528; DB 1; Length 340;
 Best Local Similarity 80.9%; Pred. No. 1,1e-143;
 Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGMEQLROEAEOLKQIDARKACADVTILAEVSGLEVGVGMQRTTTLGHLAKIYA 60
 DB 1 MSELEQLROEAEOLKQIDARKACADVTILAEVSGLEVGVGMQRTTTLGHLAKIYA 60
 QY 61 MHVATDSKLLVSAQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNN 120
 DB 61 MHMTGDSRLVSAQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNN 120
 QY 121 CSTYLNKSRGNKVSRELTAHTGYLSGCCRFDDNNITVSSGDTTCALMDIETGOQKTYF 180
 DB 121 CSTYLNKSRGNKVSRELTAHTGYLSGCCRFDDNNITVSSGDTTCALMDIETGOQKTYF 180
 QY 121 CSTYLNKSRGNKVSRELTAHTGYLSGCCRFDDNNITVSSGDTTCALMDIETGOQKTYF 180
 DB 121 CSTYLNKSRGNKVSRELTAHTGYLSGCCRFDDNNITVSSGDTTCALMDIETGOQKTYF 180
 QY 181 VGHGDCMSLAVSPDFNLFTSGACDASAKLMDVREGTCRQFTTGHSIDINAICFFPNGEA 240
 DB 181 AGHSGDVMSLAVSPDFNLFTSGACDASAKLMDVREGTCRQFTTGHSIDINAICFFPNGEA 240
 QY 241 ICTGSDASCRFLPADDELICFSHESITIGITSVAFLSGRLFAGYDDFNCNVWDSM 300
 DB 241 FTTSDDATCFLPADDELICFSHESITIGITSVAFLSGRLFAGYDDFNCNVWDSM 300
 QY 301 KSERVGIISGHDNRVSCIGVTADGMAVATGSDSFLKTN 340
 DB 301 KDRAGVLAGHDNRVSCIGVTADGMAVATGSDSFLKTN 340

RESULT 5
 US-08-190-802A-45
 Sequence 45, Application US/08190802A
 Patent No. 5519003
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Ron, Dorit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Dehlinger & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto

STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentln Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190, 802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 341 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: GTP binding protein (squid), Fig. 28
 US-08-190-802A-45

Query Match 80.9%; Score 1463; DB 1; Length 341;
 Best Local Similarity 79.0%; Pred. No. 3e-137;
 Matches 267; Conservative 32; Mismatches 39; Indels 0; Gaps 0;

QY 3 EMEQLROEAEOLKQIDARKACADVTILAEVSGLEVGVGMQRTTTLGHLAKIYAMH 62
 DB 4 ELEALRETEQLKQIDARKACADVTILAEVSGLEVGVGMQRTTTLGHLAKIYAMH 63
 QY 63 WANDSKLLVSAQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNN 122
 DB 64 WANDSKLLVSAQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNN 123
 QY 123 IYNLSKREGNVKVSRELTAHTGYLSGCCRFDDNNITVSSGDTTCALMDIETGOQKTYF 182
 DB 124 IYSLKTRGNVVSRELTAHTGYLSGCCRFDDNNITVSSGDTTCALMDIETGOQKTYF 183
 QY 183 HTGCMASLAVSPDFNLFTSGACDASAKLMDVREGTCRQFTTGHSIDINAICFFPNGEA 242
 DB 184 HTGCMASLAVSPDFNLFTSGACDASAKLMDVREGTCRQFTTGHSIDINAICFFPNGEA 243
 QY 243 TGSDASCRFLPADDELICFSHESITIGITSVAFLSGRLFAGYDDFNCNVWDSM 302
 DB 244 TGSDATCFLPADDELICFSHESITIGITSVAFLSGRLFAGYDDFNCNVWDSM 303
 QY 303 ERVGIISGHDNRVSCIGVTADGMAVATGSDSFLKTN 340
 DB 304 ERAGVLAGHDNRVSCIGVTADGMAVATGSDSFLKTN 341

RESULT 6
 US-08-190-802A-40
 Sequence 40, Application US/08190802A
 Patent No. 5519003
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Ron, Dorit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Dehlinger & Associates

```

STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0980
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G- BETA DROSOPH, Fig. 23
US-08-190-802A-40

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Query Match      80.7%; Score 1459; DB 1; Length 340;
Best Local Similarity 77.4%; Pred. No. 7.6e-137;
Matches 263; Conservative 35; Mismatches 42; Indels 0; Gaps 0;

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QY 1 MEQMQLQREAEQQLKQADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
   1 NMEQLSLQREAEKLNARDAKACDTSILQAAATSLPIGRIMRTRRLRGLAKIYA 60
QY 61 MHMATDSKLIVASASODGLIYWDSTYTNKVAHPIRBSWMTCAVYASGNFVACGGIDNM 120
   61 MHMGDSNINIVASASODGLIYWDSTYTNKVAHPIRBSWMTCAVYASGNFVACGGIDNM 120
Db 61 MHMGDSNINIVASASODGLIYWDSTYTNKVAHPIRBSWMTCAVYASGNFVACGGIDNM 120
QY 121 CSTIYMLKTRREGNVRYSRELPGHGYLSCCRFLDNNQIVTSSGDMSCGLMDIETGLQVTSF 180
   121 CSTIYMLKTRREGNVRYSRELPGHGYLSCCRFLDNNQIVTSSGDMSCGLMDIETGLQVTSF 180
Db 121 CSTIYMLKTRREGNVRYSRELPGHGYLSCCRFLDNNQIVTSSGDMSCGLMDIETGLQVTSF 180
QY 181 VGHGTDCMSLAVSPDNFLFTISGACDASAKIMDVREGTCROTFTGHESDINAICTFPNGEA 240
   181 LGHTGDVVALSLAPQCKTFEVSACDASAKIMDVREGTCROTFTGHESDINAICTFPNGEA 240
Db 181 LGHTGDVVALSLAPQCKTFEVSACDASAKIMDVREGTCROTFTGHESDINAICTFPNGEA 240
QY 241 ICTGSSDASCHFLDRADELICFHSIIICGITSVAFSLSGRLLFAGYDENCNWDNM 300
   241 FATGSDATCRFLDIRADQELAMYSHNIICGITSVAFSLSGRLLFAGYDENCNWDNM 300
Db 241 FATGSDATCRFLDIRADQELAMYSHNIICGITSVAFSLSGRLLFAGYDENCNWDNM 300
QY 301 KSERVGIISGHDNRVSCGLGYTAGMAVATGSMDSFLKIWN 340
   301 KAERSGIIAGHDNRVSCGLGYTAGMAVATGSMDSFLKIWN 340
Db 301 KAERSGIIAGHDNRVSCGLGYTAGMAVATGSMDSFLKIWN 340

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```

RESULT 7
US-08-190-802A-39
Sequence 39, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theeof
NUMBER OF SEQUENCES: 265

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0980
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G-Beta- bovine (2), Fig. 22
US-08-190-802A-39

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```

Query Match      78.6%; Score 1421; DB 1; Length 326;
Best Local Similarity 78.2%; Pred. No. 4.2e-133;
Matches 259; Conservative 29; Mismatches 33; Indels 10; Gaps 2;

```

```

QY 15 KQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYAMHMTDLSKLIVAS 74
   1 RQIADARKACGDSSTLTQITAGLDVGRIGQMRTRRLRGLAKIYAMHMTDLSKLIVAS 74
Db 1 RQIADARKACGDSSTLTQITAGLDVGRIGQMRTRRLRGLAKIYAMHMTDLSKLIVAS 74
QY 75 ODGKLIWDS-----YTNKVAHPIRBSWMTCAVYASGNFVACGGIDNMCSYIWLKSR 129
   75 ODGKLIWDS-----YTNKVAHPIRBSWMTCAVYASGNFVACGGIDNMCSYIWLKSR 129
Db 75 ODGKLIWDS-----YTNKVAHPIRBSWMTCAVYASGNFVACGGIDNMCSYIWLKSR 129
QY 130 EGNVSVRELTAHTGYLSCCRFLDNNQIVTSSGDTTCALMDIETFGQOQTVFVGHGTDCMS 189
   130 EGNVSVRELTAHTGYLSCCRFLDNNQIVTSSGDTTCALMDIETFGQOQTVFVGHGTDCMS 189
Db 130 EGNVSVRELTAHTGYLSCCRFLDNNQIVTSSGDTTCALMDIETFGQOQTVFVGHGTDCMS 189
QY 189 LAVSPDNFLFTISGACDASAKIMDVREGTCROTFTGHESDINAICTFPNGEAICTGSSDAS 249
   189 LAVSPDNFLFTISGACDASAKIMDVREGTCROTFTGHESDINAICTFPNGEAICTGSSDAS 249
Db 189 LAVSPDNFLFTISGACDASAKIMDVREGTCROTFTGHESDINAICTFPNGEAICTGSSDAS 249
QY 249 CRFLDRADELICFHSIIICGITSVAFSLSGRLLFAGYDENCNWDNMKSERVGIIS 309
   249 CRFLDRADELICFHSIIICGITSVAFSLSGRLLFAGYDENCNWDNMKSERVGIIS 309
Db 249 CRFLDRADELICFHSIIICGITSVAFSLSGRLLFAGYDENCNWDNMKSERVGIIS 309
QY 310 GHNRVSCGLGYTAGMAVATGSMDSFLKIWN 340
   310 GHNRVSCGLGYTAGMAVATGSMDSFLKIWN 340
Db 310 GHNRVSCGLGYTAGMAVATGSMDSFLKIWN 340

```

```

RESULT 8
US-09-032-372-1
Sequence 1, Application US/09032372
Patent No. 6008337
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Cortley, Neil C.

```

Query Match	52.5%;	Score 949.5;	DB 3;	Length 395;
Best Local Similarity	52.2%;	Pred. No. 3.5e-86;		
Matches 178; Conservative	56;	Mismatches 102;	Indels 5;	Gaps 3;

Db 354 VLKGSRSILFGHENRSTLKVSPDGLAFCSGSMDHLKAVN 221

Query Match	35.9%;	Score 650;	DB 1;	Length 423;
Best Local Similarity	36.8%;	Pred. No. 2.1e-56;		
Matches 141; Conservative	71;	Mismatches 125;	Indels 46;	Gaps 6.

Db : 337 QTLKSTSSSYLDNQGVSLLDFASGKLMI^{SC}I^DISCVMDV^{EN}QZVST

QY 318 LGVTADGAAVATGSDSFLKINN 340
DB 397 VRSSPDGLAVCTGSDMTKIMS 419

RESULT 10

US-08-190-802A-27
Sequence 27, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: RACK1 Amino Acid Sequence, Fig. 1C
US-08-190-802A-27

Query Match 16.9%; Score 305.5; DB 1; Length 317;
Best Local Similarity 31.5%; Pred. No. 2,2e-22;
Matches 82; Conservative 45; Mismatches 118; Indels 15; Gaps 6;

QY 48 RRTLRGHLAKTYAAHMAATDSKLVASASQDKLIYWDSTYTNKVAHAIPLRSSWVMCAVAP 107
DB 56 QRALRGSHHEFVSDVVISDQFALSGSDGTLRIMDLTGTTRRRVGHGTRKTVLSVAEVS 115
QY 108 SGNFVACGGIDNMCSYLNLSKREGNVKVSRELTAHTGYLSCCRFL--DDNNIVTSSG-DT 164
DB 116 DNRQIVSGSDTKIKLMTNL--GVCKITYODESHSEWVCVAFSPNSNPITIVSCGMDK 172
QY 165 TCALMDIETGQOKTVFVGHGDCMSLAVSPDNLFISGACDASAKLMDVREGTCROTFTG 224
DB 173 LVKVMNLANCKLTNHHGTYLNTVTSPPDSILCASGGKDGQAMLMDLNECKHLTYIDG 232
QY 225 HESDINAIICFPNGEALICGSDASCRFLDLA-----DELICFSHESIIGITSVA 277
DB 233 GDI-INALCSPRRYWLCAAT--GPSTIKIMDLGKITIVDELAKQEVISTSSKAEPPOCTSLA 290
QY 278 FSLSGRLIFAGYDDFNCNVW 297

DB 291 WSAADGOTLFAGYTDNLVRYW 310

RESULT 11

US-08-190-802A-41
Sequence 41, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G-BETA HUMAN, Fig. 24
US-08-190-802A-41

Query Match 16.9%; Score 305.5; DB 1; Length 317;
Best Local Similarity 31.5%; Pred. No. 2,2e-22;
Matches 82; Conservative 45; Mismatches 118; Indels 15; Gaps 6;

QY 48 RRTLRGHLAKTYAAHMAATDSKLVASASQDKLIYWDSTYTNKVAHAIPLRSSWVMCAVAP 107
DB 56 QRALRGSHHEFVSDVVISDQFALSGSDGTLRIMDLTGTTRRRVGHGTRKTVLSVAEVS 115
QY 108 SGNFVACGGIDNMCSYLNLSKREGNVKVSRELTAHTGYLSCCRFL--DDNNIVTSSG-DT 164
DB 116 DNRQIVSGSDTKIKLMTNL--GVCKITYODESHSEWVCVAFSPNSNPITIVSCGMDK 172
QY 165 TCALMDIETGQOKTVFVGHGDCMSLAVSPDNLFISGACDASAKLMDVREGTCROTFTG 224
DB 173 LVKVMNLANCKLTNHHGTYLNTVTSPPDSILCASGGKDGQAMLMDLNECKHLTYIDG 232
QY 225 HESDINAIICFPNGEALICGSDASCRFLDLA-----DELICFSHESIIGITSVA 277
DB 233 GDI-INALCSPRRYWLCAAT--GPSTIKIMDLGKITIVDELAKQEVISTSSKAEPPOCTSLA 290
QY 278 FSLSGRLIFAGYDDFNCNVW 297
DB 291 WSAADGOTLFAGYTDNLVRYW 310


```

1 RESULT 13
2 US-08-190-802A-62
3 ; Sequence 62, Application US/08190802A
4 ; Patent No. 5519003
5 ;
6 ; GENERAL INFORMATION:
7 ; APPLICANT: Mochly-Rosen, Daria
8 ; APPLICANT: Ron, Dorit
9 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
10 ; TITLE OF INVENTION: Thereof
11 ; NUMBER OF SEQUENCES: 265
12 ;
13 ; CORRESPONDENCE ADDRESSES:
14 ; ADDRESSEE: Denlinger & Associates
15 ; STREET: P.O. Box 60850
16 ; CITY: Palo Alto
17 ; STATE: CA
18 ; COUNTRY: USA
19 ; ZIP: 94306-0850
20 ;
21 ; COMPUTER READABLE FORM:
22 ; MEDIUM TYPE: Floppy disk
23 ; COMPUTER: IBM PC compatible
24 ; OPERATING SYSTEM: PC-DOS/MS-DOS
25 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
26 ;
27 ; CURRENT APPLICATION DATA:
28 ; APPLICATION NUMBER: US/08/190,802A
29 ; FILING DATE: 01-FEB-1994
30 ; CLASSIFICATION: 530
31 ;
32 ; ATTORNEY/AGENT INFORMATION:
33 ; NAME: Fabian, Gary R.
34 ; REGISTRATION NUMBER: 33,875
35 ; REFERENCE/DOCKET NUMBER: 8600-0139
36 ;
37 ; TELECOMMUNICATION INFORMATION:
38 ; TELEPHONE: (415) 324-0880
39 ; TELEFAX: (415) 324-0960
40 ;
41 ; INFORMATION FOR SEQ ID NO: 62:
42 ; SEQUENCE CHARACTERISTICS:
43 ; LENGTH: 704 amino acids
44 ; TYPE: amino acid
45 ; TOPOLOGY: unknown
46 ; MOLECULE TYPE: protein
47 ;
48 ; HYPOTHETICAL: NO
49 ; ANTI-SENSE: NO
50 ;
51 ; ORIGINAL SOURCE:
52 ;
53 ; INDIVIDUAL ISOLATE: TRANSCRIPTION FACTOR TTF, Fig. 45
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Query Match Similarity      16.9% ; Score 305.5, DB 1 ; Length 317;
Best Local Similarity      31.5% ; Pred. No. 2.2e-22;
Matches      82; Conservative 45; Mismatches 118; Indels 15; Gaps 6;

QY      48 RRTLRGLAKIYAMHWATSKLIVASODGKILVMPSTYTNKVAHILPLSSWVMCAVP 107
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      56 QRRLRHSHFVSDVYVSSDGQFALSSMDGTLRLMDLTGTTTRFVGHGKQVLVAESS 115
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      108 SGNFVACGGGLDMWCSLYLNKSRGNVKKYSRELSAHTGYISCCRELT--DDNNIVTSSG--DT 164
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      116 DNRQIVYSSRDKTITKILMNTL---GVCKTIVODESHSEWVSCVRFSPNSNPITVSCGMDK 172
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      165 TCALMDIEFGQQTVEVFGHTGDCMSLAVSPDNLTISGACDASAKILMPDRETCNQETFG 224
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      173 LVKVNVLNCKRTKTHTIGHTGYLNTVTFSPDGLCASGGKQGAALMDLNECKHLTYTIDG 232
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      225 HESDINAIQFPNGEAITGSDPADACRFLDRA-----DOELICFHESTILIGITSVA 277
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      233 GDI--INALCFSPNRYLCAAT--GPSIKITWDEGKIYDELKOEYVISTSKKAPQCSIA 290
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      278 FSLSGRLIFAGYDDENCNVW 297
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      291 WSAOQQTILFAGTIDNLVW 310
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

[illegible]

RESULT 14
US-08-188-582-5
; Sequence 5, Application US/08188582
; Patent No. 5534410
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 704 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-582-5

Query Match 16.4%; Score 296; DB 1; Length 704;
Best Local Similarity 27.5%; Pred. No. 6e-21;
Matches 87; Conservative 52; Mismatches 133; Indels 44; Gaps 9;

DB 55 LAKIYAMHMTDSKLVASASODGKLIWDSYTTNKVHAIPLRSSWVMCA-YAPSGNVA 113
114 CGGIDNKCSTYLN-----KSRGNV-----VSRLSAHTGYL 146
DB 345 LKIKALREAS-KRLALSKQDPSAVF---YTV-----LNSHOGVTCATLSDDSTMA 393
DB 394 CGFDSSVRIWISLTPAKLRLLKADSLRELDRKSADINRMDDRGEGVTRSLMGHTGV 453
DB 147 SCGRFLDNNIVTS-SGDTTCALMDIETGQOKTVFVGHGDCMSLAVSPDFNLFTSGACD 205
DB 454 YRCFAPEBNMLLSGSDSTIRLMSLLTWSCVYTRGHVYPVDFAPAGGYFVSCSYD 513
DB 206 ASAKLMDVRECTCRQFTGTHESDINAICTPPNGEALCTGSDDAASCFLPLRADOEL-ICF 264
DB 514 KTAFLMADSDNOALRFVGHLSDDVQVQFPHNSNYATGSSDRTVRLMDMTGOSVRLMT 573
DB 265 SHESITGCTSVASISGLRLFAGYDFDNCNVMDSKSEFVGILSGHNRVSCLGATADG 324

DB 574 GHKG---SVSLAFBACRYLASGSVDHNIIMPLNSGLVTLRLRTSVVTTTFESRDG 630
DB 325 MAVATGSMDSFLKIN 340
DB 631 TVLAAGADNNLTLMWD 646

RESULT 15
US-08-646-715-5
; Sequence 5, Application US/08646715
; Patent No. 5637686
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 704 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-715-5

Query Match 16.4%; Score 296; DB 1; Length 704;
Best Local Similarity 27.5%; Pred. No. 6e-21;
Matches 87; Conservative 52; Mismatches 133; Indels 44; Gaps 9;

DB 55 LAKIYAMHMTDSKLVASASODGKLIWDSYTTNKVHAIPLRSSWVMCA-YAPSGNVA 113
DB 345 LKIKALREAS-KRLALSKQDPSAVF---YTV-----LNSHOGVTCATLSDDSTMA 393
DB 114 CGGIDNKCSTYLN-----KSRGNV-----VSRLSAHTGYL 146
DB 394 CGFDSSVRIWISLTPAKLRLLKADSLRELDRKSADINRMDDRGEGVTRSLMGHTGV 453
DB 147 SCGRFLDNNIVTS-SGDTTCALMDIETGQOKTVFVGHGDCMSLAVSPDFNLFTSGACD 205

Fri Sep 28 10:45:11 2001

us-09-492-029-5.rai

Page 9

Db 454 YRCAPAPENMLLSCSEDSTIRLWSLLTWSCVYTYRGHVYPWVDVRAAPHGYFVSCSYD 513
Qy 206 ASAKLMDVREGTCROTETGHESDINAICFPNGEAICTGSDASCRLFDLRADOEL-ICF 264
Db 514 KTAFLMATSNOALRVFVGHLSVDVQVQFHPNSNYVATGSSDRTVRLMDNMTGQSVRLMT 573
Qy 265 SHESITCITSVAPSLGRLFAGYDDFNVCNVWDSMKSERVGLSGHNDNRVSCLGVTADG 324
Db 574 GHKG--SVSSIAFSACGRYLAGSVYDHNITLWLSNGSLVTTLLRHTSTVTTITFSRDG 630
Qy 325 MAVATGSWDSFLKIMN 340
Db 631 TVLAAGLDNNLTIMD 646

Search completed: September 28, 2001, 10:28:40
Job time: 31 sec

Fri Sep 28 10:45:14 2001

us-09-492-029-5.rpr

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:33:20 : Search time 25.94 Seconds
(without alignments)
998.433 Million cell updates/sec

Title: us-09-492-029-5
Perfect score: 1809
Sequence: 1 MGEKQRLQAEQLEKQIAD.....TADGNAVATGSDSFLKTN 340

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-68.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1809	100.0	340	1 RGHUB3	GTP-binding regula
2	1762	97.4	340	1 I53871	G-protein beta-sub
3	1578	87.2	340	1 RGHUB1	GTP-binding regula
4	1578	87.2	340	1 RGHOB1	GTP-binding regula
5	1578	87.2	340	1 JCS057	G-protein beta 1 -
6	1528	84.5	340	1 RGHUB2	hypothetical prote
7	1525	84.3	340	1 T20830	GTP-binding regula
8	1520	84.0	340	1 RGRMB	GTP-binding regula
9	1500	82.9	340	1 RGRMB4	GTP-binding regula
10	1480	81.8	341	2 S34348	GTP-binding regula
11	1469	81.2	326	1 RGOB2	GTP-binding regula
12	1463	80.9	341	1 RGOB2	GTP-binding regula
13	1459	80.7	340	1 RGRMB	GTP-binding regula
14	1238	68.4	347	1 A47370	beta-5 GTP-binding
15	948.5	52.4	353	2 A54969	hypothetical prote
16	927.5	51.3	356	2 T23478	GTP-binding regula
17	847	46.8	380	2 T03765	GTP-binding protei
18	831	45.9	380	2 T02085	GTP-binding protei
19	824	45.6	377	2 T04086	GTP-binding protei
20	822	45.4	375	2 T03256	GTP-binding protei
21	822	45.4	377	2 T07376	GTP-binding protei
22	822	45.4	377	2 T04089	GTP-binding protei
23	817	45.1	346	1 RGRMB	GTP-binding regula
24	815	45.1	377	2 T05266	GTP-binding regula
25	794	43.9	380	2 T08036	GTP-binding regula
26	790	43.7	377	2 T16985	GTP-binding protei
27	743.5	41.1	283	2 T17256	hypothetical prote
28	670	37.0	317	2 S72457	GTP-binding regula
29	668	36.9	305	2 T50474	GTP-binding regula

30	647	35.8	423	2 S60939	GTP-binding protei
31	609	33.7	123	2 S29121	GTP-binding regula
32	585.5	32.4	240	2 T02059	beta transducin-1i
33	377.5	20.9	1356	2 T18521	u4/06 snRNP 52K pr
34	308.5	17.1	465	2 A32569	probable WD-repeat
35	308	17.0	333	2 G85034	GTP-binding protei
36	305.5	16.9	317	2 A33928	GTP-binding protei
37	305.5	16.9	317	2 B33928	GTP-binding regula
38	305.5	16.9	317	2 S45054	GTP-binding regula
39	305.5	16.9	317	2 S38398	GTP-binding regula
40	305.5	16.9	317	2 A36986	activated protein
41	305.5	16.9	502	2 T41148	trp asp repeat con
42	300.5	16.6	586	2 T38992	WD-40 repeat regul
43	299.5	16.6	1693	2 S76086	beta transducin-1i
44	299	16.5	1049	2 T42045	beta transducin-1i
45	297	16.4	554	2 T02445	probable u4/06 sma

ALIGNMENTS

RESULT 1
RGHUB3
GTP-binding regulatory protein beta-3 chain - human
N:Alternate names: guanine nucleotide binding protein beta-3 chain; heterotrimeric G-
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C:Accession: A35096
R:Levine, M.A.; Smallwood, P.M.; Moen Jr., P.T.; Helman, L.J.; Ahn, T.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 2329-2333, 1990
A:Title: Molecular cloning of beta3 subunit, a third form of the G protein beta-subun
A:Reference number: A35096; MUID:90192801
A:Accession: A35096
A:Molecule type: mRNA
A:Residues: 1-340 <LEV>
A:Cross-references: GB:M31328; NID:9183412; PIDN:AAA52582.1; PID:9306776
C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
ains. The beta and gamma chains, required for GTPase activity, appear to be common to
rase; it is specific for each type of G protein.
C:Comment: In mammals, four distinct types of beta chains have been found.
C:Genetics:
A:Gene: GDB:GNB3
A:Cross-references: GDB:120005; OMIM:139130
A:Map position: 12p13-12p13
C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
C:Keywords: GTP binding; heterotrimer; signal transduction
F:51-84/Domain: WD repeat homology <WD1>
F:88-126/Domain: WD repeat homology <WD2>
F:139-171/Domain: WD repeat homology <WD3>
F:180-213/Domain: WD repeat homology <WD4>
F:222-255/Domain: WD repeat homology <WD5>
F:263-299/Domain: WD repeat homology <WD6>
F:308-340/Domain: WD repeat homology <WD7>

Query Match 100.0% Score 1809; DB 1; Length 340;
Best local similarity 100.0% Pred. No. 7.5e+145;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGEKQRLQAEQLEKQIADKARACADVTLAELVSGLEFVGRVOMRRLRLGHLAKIYA	60
DB	1	MGEKQRLQAEQLEKQIADKARACADVTLAELVSGLEFVGRVOMRRLRLGHLAKIYA	60
QY	61	MHWATDSKLLVSAOSGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM	120
DB	61	MHWATDSKLLVSAOSGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM	120
QY	121	CSITNLSKREGNVASRSLSAHTGYLSCCRFLDNNITVSSDFTTCALMDIETGQOKTVE	180
DB	121	CSITNLSKREGNVASRSLSAHTGYLSCCRFLDNNITVSSDFTTCALMDIETGQOKTVE	180
QY	181	VGHTEGDKSLAVSPDFNLFTSGACDASAKLMDVREGTCRQFTGHSIDNAICFPNGEA	240
DB	181	VGHTEGDKSLAVSPDFNLFTSGACDASAKLMDVREGTCRQFTGHSIDNAICFPNGEA	240

Db 181 VGHGDCMSLAVSPDNLFISGACDASAKLMDVREGTCQRTTGHSIDINACEFPNGEA 240
 QY 241 ICTGSDASCRFLDLRADELICFHSHESTICGITSVAFLSGRLFAGYDFFNCNWDMSM 300
 Db 241 ICTGSDASCRFLDLRADELICFHSHESTICGITSVAFLSGRLFAGYDFFNCNWDMSM 300
 QY 301 KSERVGLISGHNDNRVSCLGVTADGMAVATGSMDSFLKIMN 340
 Db 301 KSERVGLISGHNDNRVSCLGVTADGMAVATGSMDSFLKIMN 340

RESULT 2

153871

G-protein beta-subunit - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000

C:Accession: 153871

R:Ray, K.; Robishaw, J.D.

Gene 149, 337-340, 1994

A:Title: Cloning and sequencing of a rat heart cDNA encoding a G-protein beta subunit re

A:Reference number: 153871; MUID:95047499

A:Accession: 153871

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-340 <RES>

A:Cross-references: GB:L29090; NID:9456703; PIDD:AAA62620.1; PID:9456704

A:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

F:222-255/Domain: WD repeat homology <WDR>

Query Match

Best Local Similarity 97.4%; Score 1762; DB 2; Length 340;

Matches 38; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMDLRQEAOLKQIADARKACADVTALVELVSGLEVGRVOMRTTGLHAKIYA 60
 Db 1 MGEMDLRQEAOLKQIADARKACADVTALVELVSGLEVGRVOMRTTGLHAKIYA 60
 QY 61 MHMATDSKLIVASASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNVACGGIDNM 120
 Db 61 MHMATDSKLIVASASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNVACGGIDNM 120
 QY 121 CSIYNLKSREGNVKVSRELTAHGTYSCCRFLDDNNITVSSGDTTCALMDIETGQQTTF 180
 Db 121 CSIYNLKSREGNVKVSRELTAHGTYSCCRFLDDNNITVSSGDTTCALMDIETGQQTTF 180
 QY 181 VGHGDCMSLAVSPDNLFISGACDASAKLMDVREGTCQRTTGHSIDINACEFPNGEA 240
 Db 181 VGHGDCMSLAVSPDNLFISGACDASAKLMDVREGTCQRTTGHSIDINACEFPNGEA 240
 QY 241 ICTGSDASCRFLDLRADELICFHSHESTICGITSVAFLSGRLFAGYDFFNCNWDMSM 300
 Db 241 ICTGSDASCRFLDLRADELICFHSHESTICGITSVAFLSGRLFAGYDFFNCNWDMSM 300
 QY 301 KSERVGLISGHNDNRVSCLGVTADGMAVATGSMDSFLKIMN 340
 Db 301 KSERVGLISGHNDNRVSCLGVTADGMAVATGSMDSFLKIMN 340

RESULT 3

RGHUB1

GTP-binding regulatory protein beta-1 chain - human

N:Alternate names: guanine nucleotide binding protein beta-1 chain; heterotrimeric G-

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C:Accession: A24853

R:Codina, J.; Stengel, D.; Woo, S.L.C.; Birbaumer, L.

FEBS Lett. 207, 187-192, 1986

A:Title: Beta-subunits of the human liver Gs/Gi signal-transducing proteins and those of

A:Reference number: A91368; MUID:87030912

A:Accession: A24853

A:Molecule type: mRNA

A:Residues: 1-340 <COD>

A:Cross-references: GB:X04526; NID:931667; PIDD:CAA28207.1; PID:931666
 A:Experimental source: Liver
 A:Note: The authors translated the codon GAG for residues 138 and 172 as Glu
 C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
 ase; it is specific for each type of G protein.
 C:Comment: In mammals, four distinct types of beta chains have been found.

A:Gene: GDB:GNB1

A:Cross-references: GDB:119279; OMIM:139380

A:Map position: 1p36-1p31.2

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C:Keywords: GTP binding; heterotrimer; signal transduction

F:51-84/Domain: WD repeat homology <WD1>

F:88-126/Domain: WD repeat homology <WD2>

F:139-171/Domain: WD repeat homology <WD3>

F:180-213/Domain: WD repeat homology <WD4>

F:222-255/Domain: WD repeat homology <WD5>

F:263-299/Domain: WD repeat homology <WD6>

F:308-340/Domain: WD repeat homology <WD7>

Query Match

Best Local Similarity 87.2%; Score 1578; DB 1; Length 340;

Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGEMDLRQEAOLKQIADARKACADVTALVELVSGLEVGRVOMRTTGLHAKIYA 60
 Db 1 MGEMDLRQEAOLKQIADARKACADVTALVELVSGLEVGRVOMRTTGLHAKIYA 60
 QY 61 MHMATDSKLIVASASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNVACGGIDNM 120
 Db 61 MHMATDSKLIVASASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNVACGGIDNM 120
 QY 121 CSIYNLKSREGNVKVSRELTAHGTYSCCRFLDDNNITVSSGDTTCALMDIETGQQTTF 180
 Db 121 CSIYNLKSREGNVKVSRELTAHGTYSCCRFLDDNNITVSSGDTTCALMDIETGQQTTF 180
 QY 181 VGHGDCMSLAVSPDNLFISGACDASAKLMDVREGTCQRTTGHSIDINACEFPNGEA 240
 Db 181 VGHGDCMSLAVSPDNLFISGACDASAKLMDVREGTCQRTTGHSIDINACEFPNGEA 240
 QY 241 ICTGSDASCRFLDLRADELICFHSHESTICGITSVAFLSGRLFAGYDFFNCNWDMSM 300
 Db 241 ICTGSDASCRFLDLRADELICFHSHESTICGITSVAFLSGRLFAGYDFFNCNWDMSM 300
 QY 301 KSERVGLISGHNDNRVSCLGVTADGMAVATGSMDSFLKIMN 340
 Db 301 KSERVGLISGHNDNRVSCLGVTADGMAVATGSMDSFLKIMN 340

RESULT 4

RGBOB1

GTP-binding regulatory protein beta-1 chain - bovine

N:Alternate names: guanine nucleotide binding protein beta-1 chain; heterotrimeric G-

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C:Accession: A24225

R:Singh, K.; Nukada, T.; Tanabe, T.; Takahashi, H.; Noda, M.; Minamino, N.; Kangaw

FEBS Lett. 191, 235-240, 1985

A:Title: Primary structure of the beta-subunit of bovine transducin deduced from the

A:Reference number: A24225; MUID:86030675

A:Accession: A24225

A:Molecule type: mRNA

A:Residues: 1-340 <SUG>

A:Cross-references: GB:X03073

R:Song, H.K.W.; Hurley, J.B.; Hopkins, R.S.; Mike-Lye, R.; Johnson, M.S.; Doolittle,

Proc. Natl. Acad. Sci. U.S.A. 83, 2162-2166, 1986

A:Title: Repetitive segmental structure of the transducin beta subunit: homology with

A:Reference number: A25457; MUID:86177563

A:Accession: A25457

A:Molecule type: mRNA

A:Residues: 1-340 <FON>


```

Qy 1 MGENEOLRQEAEOQLKQIADARRACADVTLAELVSGLEVYGRVOMTRRTLGHAKIYA 60
  1 MSELQOLRQEAEOQLKQIADARRACADVTLAELVSGLEVYGRVOMTRRTLGHAKIYA 60
Db 1 MSELQOLRQEAEOQLKQIADARRACADVTLAELVSGLEVYGRVOMTRRTLGHAKIYA 60
Qy 61 MHWATDSKLVASQODGKLIWMDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
  61 MHWATDSKLVASQODGKLIWMDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
Db 61 MHWATDSKLVASQODGKLIWMDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
Qy 121 CSITNLSKREGNVAVSRELTAHGYLSCCRFLDDNNIVTSSGDTTCALMDITGOOKTVE 180
  121 CSITNLSKREGNVAVSRELTAHGYLSCCRFLDDNNIVTSSGDTTCALMDITGOOKTVE 180
Db 121 CSITNLSKREGNVAVSRELTAHGYLSCCRFLDDNNIVTSSGDTTCALMDITGOOKTVE 180
Qy 181 VGHGTGCMSLAVSPDNFLTSGACDASAKLMDVREGTCROTFTGHESDINACEFPNGEA 240
  181 VGHGTGCMSLAVSPDNFLTSGACDASAKLMDVREGTCROTFTGHESDINACEFPNGEA 240
Db 181 VGHGTGCMSLAVSPDNFLTSGACDASAKLMDVREGTCROTFTGHESDINACEFPNGEA 240
Qy 241 ICHGSDASCRFLDLRADELICFESHESITICITVAASLSGRLLFAGYDDPNCVWMSM 300
  241 ICHGSDASCRFLDLRADELICFESHESITICITVAASLSGRLLFAGYDDPNCVWMSM 300
Db 241 ICHGSDASCRFLDLRADELICFESHESITICITVAASLSGRLLFAGYDDPNCVWMSM 300
Qy 301 KSERVGLSGHNDNRVSCGLGTADGMAVATGWSDFLKIWN 340
  301 KSERVGLSGHNDNRVSCGLGTADGMAVATGWSDFLKIWN 340
Db 301 KSERVGLSGHNDNRVSCGLGTADGMAVATGWSDFLKIWN 340

```

```

RESULT 7
T20830
hypothetical protein F13D12.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T20830
R:Colles, L.
submitted to the EMBL Data Library, April 1995
A:Reference number: Z19330
A:Accession: T20830
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-340 <WIL>
A:Cross-references: EMBL:Z49127; P1DN:CAA88948.1; GSPDB:GN00020; CESP:F13D12.7
C:Genetics:
A:Gene: CESP:F13D12.7
A:Map position: 2
A:Introns: 19/3; 57/3; 89/3; 116/1; 166/2; 209/3; 233/3; 306/1
C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

```

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Query Match
Best Local Similarity 84.3%; Score 1525; DB 2; Length 340;
Matches 277; Conservative 29; Mismatches 34; Indels 0; Gaps 0;

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Qy 1 MGENEOLRQEAEOQLKQIADARRACADVTLAELVSGLEVYGRVOMTRRTLGHAKIYA 60
  1 MSELQOLRQEAEOQLKQIADARRACADVTLAELVSGLEVYGRVOMTRRTLGHAKIYA 60
Db 1 MSELQOLRQEAEOQLKQIADARRACADVTLAELVSGLEVYGRVOMTRRTLGHAKIYA 60
Qy 61 MHWATDSKLVASQODGKLIWMDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
  61 MHWATDSKLVASQODGKLIWMDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
Db 61 MHWATDSKLVASQODGKLIWMDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
Qy 121 CSITNLSKREGNVAVSRELTAHGYLSCCRFLDDNNIVTSSGDTTCALMDITGOOKTVE 180
  121 CSITNLSKREGNVAVSRELTAHGYLSCCRFLDDNNIVTSSGDTTCALMDITGOOKTVE 180
Db 121 CSITNLSKREGNVAVSRELTAHGYLSCCRFLDDNNIVTSSGDTTCALMDITGOOKTVE 180
Qy 181 VGHGTGCMSLAVSPDNFLTSGACDASAKLMDVREGTCROTFTGHESDINACEFPNGEA 240
  181 VGHGTGCMSLAVSPDNFLTSGACDASAKLMDVREGTCROTFTGHESDINACEFPNGEA 240
Db 181 VGHGTGCMSLAVSPDNFLTSGACDASAKLMDVREGTCROTFTGHESDINACEFPNGEA 240
Qy 241 ICHGSDASCRFLDLRADELICFESHESITICITVAASLSGRLLFAGYDDPNCVWMSM 300
  241 ICHGSDASCRFLDLRADELICFESHESITICITVAASLSGRLLFAGYDDPNCVWMSM 300
Db 241 ICHGSDASCRFLDLRADELICFESHESITICITVAASLSGRLLFAGYDDPNCVWMSM 300
Qy 301 KSERVGLSGHNDNRVSCGLGTADGMAVATGWSDFLKIWN 340
  301 KSERVGLSGHNDNRVSCGLGTADGMAVATGWSDFLKIWN 340

```

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Db 301 KSERVGLSGHNDNRVSCGLGTADGMAVATGWSDFLKIWN 340

```

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RESULT 8
RGKWB
GTP-binding regulatory protein beta chain - Caenorhabditis elegans
N:Alternate names: guanine nucleotide binding protein beta chain; heterotrimeric G-pr
C:Species: Caenorhabditis elegans
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C:Accession: S09591
R:van der Voorn, L.; Gebbink, M.; Plasterk, R.H.A.; Ploegh, H.L.
J. Mol. Biol. 213, 17-26, 1990
A:Title: Characterization of a G-protein beta-subunit gene from the nematode Caenorha
A:Reference number: S09591; MUID:90250769
A:Accession: S09591
A:Molecule type: DNA
A:Residues: 1-340 <VAN>
A:Cross-references: EMBL:X17497; NID:96642; P1DN:CAA35532.1; PID:96643
C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
ase; it is specific for each type of G protein.
C:Comment: In mammals, four distinct types of beta chains have been found.
C:Genetics:
A:Introns: 19/3; 57/3; 89/3; 115/2; 166/1; 209/3; 233/3; 305/2
C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
C:Keywords: GTP binding; heterotrimer; signal transduction
F:51-84/Domain: WD repeat homology <WD1>
F:88-126/Domain: WD repeat homology <WD2>
F:139-171/Domain: WD repeat homology <WD3>
F:180-213/Domain: WD repeat homology <WD4>
F:222-255/Domain: WD repeat homology <WD5>
F:263-299/Domain: WD repeat homology <WD6>
F:308-340/Domain: WD repeat homology <WD7>

```

```

Query Match
Best Local Similarity 84.0%; Score 1520; DB 1; Length 340;
Matches 276; Conservative 29; Mismatches 35; Indels 0; Gaps 0;

```

```

Qy 1 MGENEOLRQEAEOQLKQIADARRACADVTLAELVSGLEVYGRVOMTRRTLGHAKIYA 60
  1 MSELQOLRQEAEOQLKQIADARRACADVTLAELVSGLEVYGRVOMTRRTLGHAKIYA 60
Db 1 MSELQOLRQEAEOQLKQIADARRACADVTLAELVSGLEVYGRVOMTRRTLGHAKIYA 60
Qy 61 MHWATDSKLVASQODGKLIWMDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
  61 MHWATDSKLVASQODGKLIWMDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
Db 61 MHWATDSKLVASQODGKLIWMDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
Qy 121 CSITNLSKREGNVAVSRELTAHGYLSCCRFLDDNNIVTSSGDTTCALMDITGOOKTVE 180
  121 CSITNLSKREGNVAVSRELTAHGYLSCCRFLDDNNIVTSSGDTTCALMDITGOOKTVE 180
Db 121 CSITNLSKREGNVAVSRELTAHGYLSCCRFLDDNNIVTSSGDTTCALMDITGOOKTVE 180
Qy 181 VGHGTGCMSLAVSPDNFLTSGACDASAKLMDVREGTCROTFTGHESDINACEFPNGEA 240
  181 VGHGTGCMSLAVSPDNFLTSGACDASAKLMDVREGTCROTFTGHESDINACEFPNGEA 240
Db 181 VGHGTGCMSLAVSPDNFLTSGACDASAKLMDVREGTCROTFTGHESDINACEFPNGEA 240
Qy 241 ICHGSDASCRFLDLRADELICFESHESITICITVAASLSGRLLFAGYDDPNCVWMSM 300
  241 ICHGSDASCRFLDLRADELICFESHESITICITVAASLSGRLLFAGYDDPNCVWMSM 300
Db 241 ICHGSDASCRFLDLRADELICFESHESITICITVAASLSGRLLFAGYDDPNCVWMSM 300
Qy 301 KSERVGLSGHNDNRVSCGLGTADGMAVATGWSDFLKIWN 340
  301 KSERVGLSGHNDNRVSCGLGTADGMAVATGWSDFLKIWN 340
Db 301 KSERVGLSGHNDNRVSCGLGTADGMAVATGWSDFLKIWN 340

```

```

RESULT 9
RGKWB4
GTP-binding regulatory protein beta-4 chain - mouse
N:Alternate names: guanine nucleotide binding protein beta-4 chain; heterotrimeric G-
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C:Accession: J50669
R:Von Weizsaecker, E.; Stratmann, M.P.; Simon, M.I.
Biochem. Biophys. Res. Commun. 183, 350-356, 1992

```


Db 1 RNOIRDAKACGSDTLNQTITAGIDPVGRIOMRTTRRLRGLAKIYAMHMCTDSRLIVSAS 60
 QY 75 QDGKLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNVPACGIDNMCSITNLSREGNWK 134
 Db 61 QDGKLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNVPACGIDNMCSITNLSREGNWK 120
 QY 135 VSRLSHHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQKRTVFGHGTDCMSIAVSP 194
 Db 121 VSRLSHHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQKRTVFGHGTDCMSIAVSP 180
 QY 195 DPNFISGADASAKIMDVREGTCRQTFGHESDINACIFPENGALCTGSDASCRLED 254
 Db 181 DGRFTVSGADASAKIMDVREGTCRQTFGHESDINACIFPENGALCTGSDATCRLED 240
 QY 255 LRADQELICSHESIIGITSVAFLSGRLIFAGYDDFNQCNWMSKSEPVGILSGHNR 314
 Db 241 LRADQELIMSHDNIIGITSVAFLSGRLLAGYDDFNQCNWMDAKGRAGVLASHDNR 300
 QY 315 VSCLGVTADGMNAVATGSMDSFLKIWN 340
 Db 301 VSCLGVTADGMNAVATGSMDSFLKIWN 326

RESULT 12

RGOORF

GMP-binding regulatory protein beta chain - northern European squid

N:Alternate names: guanine nucleotide binding protein beta chain; heterotrimeric G-protein
 C:Species: Loligo forbesi (northern European squid)
 C:date: 31-Dec-1992 #sequence-revision 31-Dec-1992 #text-change 22-Jun-1999

R:Accession: S13302

R:Ryba, N.J.P.; Pottinger, J.D.D.; Keen, J.N.; Findlay, J.B.C.
 Biochem. J. 273. 225-228, 1991

A:Title: Sequence of the beta subunit of the phosphatidylinositol-specific phospholipase
 A:Reference number: S13302; MUID:9113146

A:Accession: S13302

A:Molecule type: mRNA

A:Residues: 1-341 <RYB>

A:Cross-references: EMBL:X56757; NID:g9507; PIDN:CAA40077.1; PID:g9508

C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
 rates. The beta and gamma chains, required for GTPase activity, appear to be common to all
 rates. It is specific for each type of G protein.

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 C:Keywords: GTP binding; heterotrimer; signal transduction

F:52-85/Domain: WD repeat homology <WD2>

F:89-127/Domain: WD repeat homology <WD3>

F:140-172/Domain: WD repeat homology <WD3>

F:181-214/Domain: WD repeat homology <WD4>

F:223-256/Domain: WD repeat homology <WD5>

F:264-300/Domain: WD repeat homology <WD6>

F:309-341/Domain: WD repeat homology <WD7>

Query Match 80.9%; Score 1463; DB 1; Length 341;
 Best Local Similarity 79.0%; Pred. No. 1e-115;

Matches 267; Conservative 32; Mismatches 39; Indels 0; Gaps 0;

QY 3 EHEOIRAEOLKQKQIADARKKADVTALVLSGLEVGRVOMRTTRRLRGLAKIYAMH 62
 Db 4 EHEOIRAEOLKQKQIADARKKADVTALVLSGLEVGRVOMRTTRRLRGLAKIYAMH 63
 QY 63 WATDSKLIVASASQDGKLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNVPACGIDNMCS 122
 Db 64 WATDSKLIVASASQDGKLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNVPACGIDNMCS 123
 QY 123 IYNLKSREGNVAKVSRELTAHHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQKRTV 182
 Db 124 IYNLKSREGNVAKVSRELTAHHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQKRTV 183
 QY 183 HTGDCMSIAVSPDNFLFTSGACDASAKIMDVREGTCRQTFGHESDINACIFPENGALIC 242
 Db 184 HTGDCMSIAVSPDNFLFTSGACDASAKIMDVREGTCRQTFGHESDINACIFPENGALIC 243
 QY 243 TGSDDASCRLEDLRADQELICSHESIIGITSVAFLSGRLLAGYDDFNQCNWMDAKGR 302

Db 244 TGSDDATCRLEDLRADQELIMSHDNIIGITSVAFLSGRLLAGYDDFNQCNWMDVILKQ 303
 QY 303 ERVGLISGHDRNVSCLGVTADGMNAVATGSMDSFLKIWN 340
 Db 304 ERVGLISGHDRNVSCLGVTADGMNAVATGSMDSFLKIWN 341

RESULT 13

RGEFBI

GMP-binding regulatory protein beta chain homolog - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
 C:date: 31-Dec-1992 #sequence-revision 31-Dec-1992 #text-change 22-Jun-1999

R:Accession: A40489

R:Rafitz, S.; Provost, N.M.; Hurley, J.B.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7134-7138, 1988

A:Title: Cloning of a Drosophila melanogaster guanine nucleotide regulatory protein b

A:Reference number: A40489; MUID:89017152

A:Accession: A40489

A:Molecule type: mRNA

A:Residues: 1-340 <YAR>

A:Cross-references: GB:M22567; GB:J04083; NID:g157497; PIDN:AAB59247.1; PID:g157498

A:Genetics:

A:Gene: FlyBase:Gabyr

A:Cross-references: FlyBase:FBgn0001105

A:Map position: X13F

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

F:51-84/Domain: WD repeat homology <WD1>

F:88-126/Domain: WD repeat homology <WD2>

F:139-171/Domain: WD repeat homology <WD3>

F:180-213/Domain: WD repeat homology <WD4>

F:222-255/Domain: WD repeat homology <WD5>

F:263-299/Domain: WD repeat homology <WD6>

F:308-340/Domain: WD repeat homology <WD7>

Query Match 80.7%; Score 1459; DB 1; Length 340;
 Best Local Similarity 77.4%; Pred. No. 2.3e-115;

Matches 263; Conservative 35; Mismatches 42; Indels 0; Gaps 0;

QY 1 MGEEOIRAEOLKQKQIADARKKADVTALVLSGLEVGRVOMRTTRRLRGLAKIYAMH 60
 Db 1 MGEEOIRAEOLKQKQIADARKKADVTALVLSGLEVGRVOMRTTRRLRGLAKIYAMH 60
 QY 61 MHWATDSKLIVASASQDGKLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNVPACGIDNM 120
 Db 61 MHWATDSKLIVASASQDGKLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNVPACGIDNM 120
 QY 121 CSYINLKSREGNVAKVSRELTAHHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQKRTV 180
 Db 121 CSYINLKSREGNVAKVSRELTAHHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQKRTV 180
 QY 181 VGHGDCMSIAVSPDNFLFTSGACDASAKIMDVREGTCRQTFGHESDINACIFPENGALIC 240
 Db 181 VGHGDCMSIAVSPDNFLFTSGACDASAKIMDVREGTCRQTFGHESDINACIFPENGALIC 240
 QY 241 ICTGSDASCRLEDLRADQELICSHESIIGITSVAFLSGRLLAGYDDFNQCNWMDAKGR 300
 Db 241 ICTGSDASCRLEDLRADQELICSHESIIGITSVAFLSGRLLAGYDDFNQCNWMDAKGR 300
 QY 301 KSEVAVGLISGHDRNVSCLGVTADGMNAVATGSMDSFLKIWN 340
 Db 301 KSEVAVGLISGHDRNVSCLGVTADGMNAVATGSMDSFLKIWN 340

RESULT 14

A47370

GTP-binding regulatory protein beta chain - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum
 C:date: 16-Feb-1994 #sequence-revision 18-Nov-1994 #text-change 13-Aug-1999

R:Accession: A47370

R:Alilly, P.; Wu, L.; Welker, D.L.; Devreotes, P.N.
 Genes Dev. 7, 986-995, 1993

A:Title: A G-protein beta-subunit is essential for Dictyostelium development.
 A:Reference number: A47370; MUID:93279474
 A:Accession: A47370
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-347 <LTL>
 A:Cross-references: GB:473641; NID:9460980; PIDN:CAA52018.1; PID:9460981
 A:Note: sequence extracted from NCBI backbone (NCBIN:132987, NCBIN:132989, NCBIN:132991, F:146-178/Domain: WD repeat homology <WD2> F:167-220/Domain: WD repeat homology <WD3> F:273-306/Domain: WD repeat homology <WD5> F:315-347/Domain: WD repeat homology #status atypical <WD6>

Query Match
 Best Local Similarity 68.4%; Score 1238; DB 2; Length 347;
 Matches 226; Conservative 47; Mismatches 64; Indels 2; Gaps 1;
 QY 3 EMEQLQEAQLKQIADARKACADVTALVSLGVVGRVQ--MRTTRTLGHLAKIYA 60
 Db 8 KIQARDESMKEQIRANRDVNDTTLKTFTRDLPGLPKKEGKIKVRNLKGLAKIYA 67
 QY 61 MHWATDSKLIVSASODGKLIWDSYTNKVAHPLRSSWMTCAVAPSGNFVACGGLDNM 120
 Db 68 MHWEDNVHLVSSODGKLIWDSGLTNKVAHPLRSSWMTCAVAPSGNFVACGGLDNM 127
 QY 121 CSTYNLKSREGVAVKSRSLAHTGYLSCCRFLDNNIYSSGDTTCALMDIETGOOKTVF 180
 Db 128 CSTYNLKSREGVAVKSRSLAHTGYLSCCRFLDNNIYSSGDTTCALMDIETGOOKTVF 187
 QY 181 VGHITGD--CNSLAVSPDNLFISGACDASAKLMDVREGTCRQTFTHESDINAICFPNGA 240
 Db 188 SDHNGDVSVSPDNLFISGACDASAKLMDVREGTCRQTFTHESDINAICFPNGA 247
 QY 241 ICTGSDASCRFLRADQELICFSHESITGITSVAFLSGRLIFAGYDDFNQWDSM 300
 Db 248 FGTGSDASCRFLRADQELICFSHESITGITSVAFLSGRLIFAGYDDFNQWDSM 307
 QY 301 KSERVGLISGHDNRVSCIGVADGMAVATGSMDFLKIW 339
 Db 308 KGERVLSLTGHNVRVSCIGVADGMAVATGSMDFLKIW 346

RESULT 15
 A54969
 beta5 GTP-binding protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 13-Aug-1999
 C:Accession: A54969
 R:Watson, A.J.; Katz, A.; Simon, M.I.
 J. Biol. Chem. 269, 22150-22156, 1994
 A:Title: A fifth member of the mammalian G-protein beta-subunit family. Expression in br
 A:Reference number: A54969; MUID:94350964
 A:Accession: A54969
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-353 <WAT>
 A:Cross-references: GB:L34290; NID:91337255; PIDN:AAA93084.1; PID:9557738
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F:59-92/Domain: WD repeat homology <WD1>
 F:149-182/Domain: WD repeat homology <WD3>
 F:193-226/Domain: WD repeat homology <WD4>
 F:279-312/Domain: WD repeat homology <WD5>
 F:321-353/Domain: WD repeat homology #status atypical <WD7>

Query Match
 Best Local Similarity 52.4%; Score 948.5; DB 2; Length 353;
 Matches 177; Conservative 57; Mismatches 102; Indels 5; Gaps 3;
 QY 4 MEQLQEAQLKQIADARKACADVTALVSLGVVGRVQ--MRTTRTLGHLAKIYAMHW 63
 Db 11 MEQLQEAQLKQIADARKACADVTALVSLGVVGRVQ--MRTTRTLGHLAKIYAMHW 63

Db 12 LASLSEASLSKGLIEERAKLHVEHLQVAREVEALGQFVMKTRTLKGNKVLCLMDM 71
 QY 64 ATDSKLIVSASODGKLIWDSYTNKVAHPLRSSWMTCAVAPSGNFVACGGLDNMCSI 123
 Db 72 CKDKRRIVSSODGKLIWDSYTNKVAHPLRSSWMTCAVAPSGNFVACGGLDNMCSI 131
 QY 124 YNL--KSHREGVAVKSRSLAHTGYLSCCRFLD--DNNIYSSGDTTCALMDIETGOOKTVF 180
 Db 132 YPLTFDKRNNMAAKKSVAMHTNLSACSFNTSDMOILIASGDTTCALMDVDSGGLDSF 191
 QY 181 VGHITGD--CNSLAVSPDNLFISGACDASAKLMDVREGTCRQTFTHESDINAICFPNG 238
 Db 192 HGHGADVLCIDLAPSETGNTFVSGGCDKRAMVDMNSGCVQAFETHESDVNSVRYPSG 251
 QY 239 EATGSDASCRFLRADQELICFSHESITGITSVAFLSGRLIFAGYDDFNQWDSM 298
 Db 252 DAFASGSDATCRFLRADQELICFSHESITGITSVAFLSGRLIFAGYDDFNQWDSM 311
 QY 299 SMKSERVGLISGHDNRVSCIGVADGMAVATGSMDFLKIW 339
 Db 312 VLKGSRYSLTGHENRVTSLRYSPOGTAFCSGMDHTLRW 352

Search completed: September 28, 2001, 10:33:21
 Job time: 272 sec

Fri Sep 28 10:45:14 2001

us-09-492-029-5.rpt

Page 8

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 28, 2001, 10:34:28 ; Search time 16.71 Seconds
(without alignments)
697.000 Million cell updates/sec

Title: US-09-492-029-5

Perfect score: 1809

Sequence: 1 MGEMEQLEQAEQLEKQAD.....TADGMAVATGSMDSFLKTIWN 340

Scoring table: BLOSUM62

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	1809	100.0	340	1	GBB3_HUMAN
2	1763	97.5	340	1	GBB3_MOUSE
3	1762	97.4	340	1	GBB3_RAT
4	1759	97.2	340	1	GBB3_CANFA
5	1578	87.2	340	1	GBB1_HUMAN
6	1573	87.0	340	1	GBB1_XENLA
7	1572	86.9	340	1	GBB1_RAT
8	1528	84.5	340	1	GBB2_HUMAN
9	1521	84.1	340	1	GBB2_MOUSE
10	1520	84.0	340	1	GBB1_CAEL
11	1500	82.9	340	1	GBB2_RAT
12	1500	82.9	340	1	GBB4_MOUSE
13	1480	81.8	340	1	GBB1_MOUSE
14	1479	81.8	340	1	GBB1_HOMAM
15	1469	81.2	340	1	GBB2_BOVIN
16	1463	80.9	340	1	GBB1_LOFLO
17	1459	80.7	340	1	GBB1_DROME
18	1238	68.4	347	1	GBB1_DICDI
19	1198	66.2	359	1	GBB1_CRYPA
20	949.5	52.5	333	1	GBB5_HUMAN
21	948.5	52.4	333	1	GBB5_MOUSE
22	927.5	51.3	356	1	GBB5_MOUSE
23	847	46.8	380	1	GBB5_MOUSE
24	831	45.9	380	1	GBB1_MOUSE
25	824	45.6	377	1	GBB1_MOUSE
26	822	45.4	375	1	GBB3_MOUSE
27	822	45.4	377	1	GBB2_MOUSE
28	822	45.4	377	1	GBB2_MOUSE
29	815	45.1	377	1	GBB2_MOUSE
30	808	44.7	346	1	GBB1_MOUSE
31	790	43.7	377	1	GBB1_MOUSE
32	668	36.9	305	1	GBB1_MOUSE
33	647	35.8	423	1	GBB1_MOUSE

ALIGNMENTS

RESULT ID	GBB3_HUMAN	STANDARD	PRT	340 AA.
AC	P16520:			
DT	01-AUG-1990 (rel. 15, Created)			
DT	01-AUG-1990 (rel. 15, Last sequence update)			
DT	01-OCT-2000 (rel. 40, Last annotation update)			
DE	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3			
DE	(TRANSDUCIN BETA CHAIN 3).			
GN	GBB3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=90192801; PubMed=2107550;			
RA	Levine M.A., Smallwood P.M., Moen P.T., Helman L.J., Ahn T.G.;			
RT	"Molecular cloning of beta 3 subunit, a third form of the G protein			
RT	beta-subunit polypeptide."			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:2329-2333(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=96303695; PubMed=8723724;			
RA	Anasari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E.;			
RA	Spanos S., Malley T., Gibbs R.A.;			
RT	"A gene-rich cluster between the CD4 and triosephosphate isomerase			
RT	genes at human chromosome 12p13."			
RT	Genome Res. 6:314-326(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Busch S., Dyhr W., Siffert W.;			
RA	Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.			
RL	- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE			
CC	INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE			
CC	SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE			
CC	GNTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-			
CC	EFFECTOR INTERACTION.			
CC	- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).			
CC	- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M1328; AAA52582.1; -			000808 podospora a
DR	EMBL; U47924; AAB51313.1; -			P49695 thermomomom
DR	EMBL; Y12050; CAA72779.1; -			P20053 saccharomyc
DR	EMBL; Y12051; CAA72779.1; -			O42248 brachydanio
DR	EMBL; Y12052; CAA72779.1; JOINED.			P23388 homo sapien
DR	EMBL; Y12053; CAA72779.1; JOINED.			O93318 drosophila
DR	EMBL; Y12054; CAA72779.1; JOINED.			O42249 oreochromis
DR	EMBL; Y12055; CAA72779.1; JOINED.			O94775 trypanosoma
DR	EMBL; Y12056; CAA72779.1; JOINED.			O55563 synchocyst
DR	EMBL; Y12057; CAA72779.1; JOINED.			O22212 arabidopsis
DR	EMBL; Y12058; CAA72779.1; JOINED.			P49846 drosophila

DR EMBL: Y12055; CAA72779.1; JOINED.
 DR EMBL: Y12056; CAA72779.1; JOINED.
 DR EMBL: Y12057; CAA72779.1; JOINED.
 DR EMBL: Y12058; CAA72779.1; JOINED.
 DR EMBL: U47930; AAC50468.1; -.
 DR PIR: A35096; KGHUB3.
 DR HSSP: P04901; 1TRB.
 DR MIM: 139130; -.
 DR InterPro: IPR001632; -.
 DR InterPro: IPR001680; -.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINBPT.
 DR PROSITE: PS00678; WD_REPEATS_1; 3.
 DR PROSITE: PS50082; WD_REPEATS_2; 5.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37221 MW; 896E706A61BD74F CRC64;

Query Match 100.0%; Score 1809; DB 1; Length 340;
 Best Local Similarity 100.0%; Pred. No. 1,5e-152;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMQLRQEAQLKQIADARKACADYTLAEVSGLEVGRVOMRTRTLRLGLAKIYA 60
 DB 1 MGEMQLRQEAQLKQIADARKACADYTLAEVSGLEVGRVOMRTRTLRLGLAKIYA 60
 QY 61 MHWAIDSKLLVASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 DB 61 MHWAIDSKLLVASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 QY 121 CSTYNLKSRGNKVSRELTAHTGYLSCCRFLDNNIYVSSGDTTCALMDIETGOQKTF 180
 DB 121 CSTYNLKSRGNKVSRELTAHTGYLSCCRFLDNNIYVSSGDTTCALMDIETGOQKTF 180
 QY 181 VGHGTGCMSLAVSPDNLFISGACDASAKIMDVREGTCRQFTGHSIDINAIICFPNGEA 240
 DB 181 VGHGTGCMSLAVSPDNLFISGACDASAKIMDVREGTCRQFTGHSIDINAIICFPNGEA 240
 QY 241 ICTGSDASCRFLDLRADELICFSHESIICGITSVAFSLSGRLLFAGYDDEFCNVWDSM 300
 DB 241 ICTGSDASCRFLDLRADELICFSHESIICGITSVAFSLSGRLLFAGYDDEFCNVWDSM 300
 QY 301 KSERVGIILSHGDNRSCLGVTADGMVAATGSMDSFLKIMN 340
 DB 301 KSERVGIILSHGDNRSCLGVTADGMVAATGSMDSFLKIMN 340

RESULT 2

GBB3_MOUSE

ID GBB3_MOUSE STANDARD: PRT; 340 AA.

AC 061011; 15-JUL-1998 (rel. 36, Created)

DT 30-MAY-2000 (rel. 39, Last sequence update)

DE 30-MAY-2000 (rel. 39, Last annotation update)

DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3

DE (TRANSDUCIN BETA CHAIN 3).

GN GNB3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,

RA Lu J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W.,
 RA Gibbs R.A.;
 RA Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 199-301 FROM N.A.
 RC STRAIN-CF-1 / HARLAN; TISSUE-Retina;
 RX MEDLINE=97011591; PubMed=8858601;
 RA Williams C.J., Schultz R.M., Kopf G.S.;
 RT "g protein gene expression during mouse oocyte growth and maturation,
 RT and preimplantation embryo development.";
 RL Mol. Reprod. Dev. 44:315-323(1996).
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSDUCER
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC RECEPTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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DR EMBL: AC002397; AAC36013.1; -.
 DR EMBL: U38494; AAB01725.1; -.
 DR HSSP: P04901; 1GP2.
 DR MGD: MGI:95785; Gnb3.
 DR InterPro: IPR001632; -.
 DR InterPro: IPR001680; -.
 DR Pfam: PF00400; WD40; 2.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINBPT.
 DR PROSITE: PS00678; WD_REPEATS_1; 3.
 DR PROSITE: PS50082; WD_REPEATS_2; 5.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37240 MW; 44BA0F8C0FDEDEB1 CRC64;

Query Match 97.5%; Score 1763; DB 1; Length 340;
 Best Local Similarity 97.1%; Pred. No. 1.7e-148;
 Matches 330; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGEMQLRQEAQLKQIADARKACADYTLAEVSGLEVGRVOMRTRTLRLGLAKIYA 60
 DB 1 MGEMQLRQEAQLKQIADARKACADYTLAEVSGLEVGRVOMRTRTLRLGLAKIYA 60
 QY 61 MHWAIDSKLLVASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 DB 61 MHWAIDSKLLVASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 QY 121 CSTYNLKSRGNKVSRELTAHTGYLSCCRFLDNNIYVSSGDTTCALMDIETGOQKTF 180
 DB 121 CSTYNLKSRGNKVSRELTAHTGYLSCCRFLDNNIYVSSGDTTCALMDIETGOQKTF 180
 QY 181 VGHGTGCMSLAVSPDNLFISGACDASAKIMDVREGTCRQFTGHSIDINAIICFPNGEA 240
 DB 181 VGHGTGCMSLAVSPDNLFISGACDASAKIMDVREGTCRQFTGHSIDINAIICFPNGEA 240
 QY 241 ICTGSDASCRFLDLRADELICFSHESIICGITSVAFSLSGRLLFAGYDDEFCNVWDSM 300
 DB 241 ICTGSDASCRFLDLRADELICFSHESIICGITSVAFSLSGRLLFAGYDDEFCNVWDSM 300

0y	301	KSERVGLISGHDNRVSLCGLVTADGAAVATGSDMSFLKTTN	340
	1		
Db	301	KCERVGLISGHDNRVSLCGLVTADGAAVATGSDMSFLKTTN	340
	3		
GBB3_RAT			
ID	GBB3_RAT	STANDARD:	PRT: 340 AA.
AC	P52287		
DT	01-OCT-1996	(Rel. 34, Created)	
DT	01-OCT-1996	(Rel. 34, Last sequence update)	
DT	15-JUL-1998	(Rel. 36, Last annotation update)	
DE	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3 (TRANSUDUCIN BETA CHAIN 3).		
DE	GNB3.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116.		
RA	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=Heart;		
RX	MEDLINE=95047499; PubMed=7959013;		
RT	Ray K., Robishaw J.D.;		
RT	"Cloning and sequencing of a rat heart cDNA encoding a G-protein beta subunit related to the human retinal beta 3 subunit.";		
RL	Gene 149:337-340(1994).		
CC	-1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.		
CC	-1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).		
CC	-1- TISSUE SPECIFICITY: EXPRESSED AT A HIGH LEVEL IN THE HEART AND AT A MUCH LOWER LEVEL IN THE BRAIN.		
CC	-1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch .		
CC	-----		
DR	EMBL: L29090: AAA62620.1; -.		
DR	HSSP: P04901: ITBG.		
DR	InterPro: IPR001632; -.		
DR	InterPro: IPR001680; -.		
DR	Pfam: PF00400: WD40; 7.		
DR	PRINTS: PR00319: GPROTEINB.		
DR	PRINTS: PR00320: GPROTEINBPT.		
DR	PROSITE: PS00678; WD_REPEATS_1; 3.		
DR	PROSITE: PS50082; WD_REPEATS_2; 5.		
DR	PROSITE: PS50294; WD_REPEATS_REGION; 1.		
KW	Transducer; Repeat; WD repeat; Multigene family.		
FT	REPEAT	53 83	WD 1.
FT	REPEAT	95 125	WD 2.
FT	REPEAT	141 170	WD 3.
FT	REPEAT	182 212	WD 4.
FT	REPEAT	224 254	WD 5.
FT	REPEAT	268 298	WD 6.
FT	REPEAT	310 340	WD 7.
SO	SEQUENCE	340 AA; 37180 MW; 020AA1E754E8BIDA	CRC64;

	Query Match	97.4%;	Score 1762;	DB 1;	Length 340;
	Best Local Similarity	96.5%;	Pred. No. 2,1e+18;		
	Matches 328; Conservative	8;	Mismatches 4;	Indels 0;	Gaps 0;
Oy	1 MGEMLQRLQEAQLKKOTADARKACADVTLAEVLVSGLEVGNGVMRTGTRILRGHLAKIYA	60			
	: : : : : : : : : : : :				

```

Db      1  MCEMQQLKOEAFOLKKQJADARKACADITTLAEIVSLGEVGRVQKRTTRRLRGLHAKIYA  60
Qy      61  MHMWTDSKLYSASODGKLIYWDSTTTKKVHAIPLRSSWMTCAAPSGNVVACGGIDNM  120
Db      61  MHMWTDSKLYSASODGKLIYWDSTTTKKVHAIPLRSSWMTCAAPSGNVVACGGIDNM  120
Qy      121  CSIYMLKREGVWVKVSRRELSAHTGTLSCRRFLDDNNITYSSGDTTCALMDIETGQOKTVE  180
Db      121  CSIYMLKREGVWVKVSRRELSAHTGTLSCRRFLDDNNITYSSGDTTCALMDIETGQOKTVE  180
Qy      181  VGHTEDCMSLAVSPDENLFIISGACDASAKLMDVREGTCRQFTFGHESDINAIICEFPNGEA  240
Db      181  VGHTEDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTFGHESDINAIICEFPNGEA  240
Qy      241  ICTGSDDASCRFLFDRAQDELICFESHETIGITSVAFLSGRLLFAGYDFPNCWYDMSM  300
Db      241  ICTGSDDASCRFLFDRAQDELITAYSHESIIGITSVAFLSGRLLFAGYDDFNCWYDMSL  300
Qy      301  KSERVGIISGHDRVSCLGVTADGAAYVNGSMDSPFLKTMN  340
Db      301  KSERVGIISGHDRVSCLGVTADGAAYVNGSMDSPFLKTMN  340

RESULT      4
GBB3_CANFA  STANDARD:      PRT:      340 AA.
ID      GBB3_CANFA  P79147.
AC      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      GUANINE NUCLEOTIDE-BINDING PROTEIN G(II)/G(s)/G(T) BETA SUBUNIT 3
DE      (TRANSDUCIN BETA CHAIN 3).
GN      GNB3.
OS      Canis familiaris (Dog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_OX  NCBI_TaxID=9615;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ALASKAN MALAMUTE; TISSUE=Retina;
RX      MEDLINE=97409956; PubMed=926671;
RA      Akhmedov N.B., Pirtiev N.I., Ray K., Acland G.M., Aguirre G.D.,
RA      Father D.B.;
RT      "Structure and analysis of the transducin beta2-subunit gene, a
RT      candidate for inherited cone degeneration (cd) in the dog.";
RL      Gene 194:47-56(1997).
CC      -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC      INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
CC      SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC      GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC      EFFECTOR INTERACTION.
CC      -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC      -1- SIMILARITY: CONTAINS 7 WD REPEATS (WRP-ASP DOMAINS).
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL, U52916; AAC48760.1; -.
DR      HSSP; P04901; 1TBG.
DR      InterPro: IPR001632; -.
DR      InterPro: IPR001680; -.
DR      Pfam; PF00400; WD40; 7.
DR      PRINTS; PR00319; GPROTEINB.
DR      PRINTS; PR00320; GPROTEINBRPT.
DR      PROSITE; PS00678; WD_REPEATS_1; 3.
DR      PROSITE; PS00682; WD_REPEATS_2; 5.
DR      PROSITE; PS02944; WD_REPEATS_REGION; 1.
KW      Transducer; Repeat; WD repeat; Multigene family.

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RESULT 4
GBB3_CANFA
ID GBB3_CANFA STANDARD: PRT: 340 AA.
AC P79147;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3
DE (TRANSDUCIN BETA CHAIN 3).
GN GNB3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid:9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ALASKAN MALAMUTE; TISSUE=Retina;
RX MEDLINE=97409956; PubMed=9266671;
RA Akhmedov N.B., Plitiev N.I., Ray K., Acland G.M., Aguirre G.D.,
RA Father D.B.;
RT "Structure and analysis of the transducin beta-subunit gene, a
RT candidate for inherited cone degeneration (cd) in the dog.";
RL Gene 194:47-56(1997).
CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC EFECTOR INTERACTION.
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (RRP-ASP DOMAINS).
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U52916; AAC48760.1; -.
CC HSSP: P04901; 1TBG.
CC InterPro: IPR001632; -.
CC InterPro: IPR001680; -.
CC Pfam: PF00400; WD40; 7.
CC PRINTS: PR00319; GPROTEINB.
CC PRINTS: PR00320; GPROTEINBRPT.
CC PROSITE: PS00678; WD_REPEATS_1; 3.
CC PROSITE: PS50082; WD_REPEATS_2; 5.
CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
CC Transducer; Repeat; WD repeat; Multigene family.
KW

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FT REPEAT 53 83 WD 1.
FT REPEAT 95 125 WD 2.
FT REPEAT 141 170 WD 3.
FT REPEAT 182 212 WD 4.
FT REPEAT 224 254 WD 5.
FT REPEAT 268 298 WD 6.
FT REPEAT 310 340 WD 7.
SQ SEQUENCE 340 AA; 37144 MW; 8E3B5A5238E29C37 CRC64;

Query Match 97.2%; Score 1759; DB 1; Length 340;
Best Local Similarity 96.8%; Pred. No. 3,9e-148;
Matches 329; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGMEQLROBAEOLKQIADARKACADVTLLAEVSGLEVGRQMTTRTLRLHAKIYA 60
D 1 MGMEQLROBAEOLKQIADARKACADVTLLAEVSGLEVGRQMTTRTLRLHAKIYA 60
QY 61 MHMATSCLKVSAODGKLIVMDSYTTNKVHAIPLRSSWMTCAPAPSGNFVACGLDMM 120
D 61 MHMATSCLKVSAODGKLIVMDSYTTNKVHAIPLRSSWMTCAPAPSGNFVACGLDMM 120
QY 121 CSTYNRKRGKNGKVSRELSAHTGYLSGCRFLDDNNIVTSSGDTTCALMDIETGQOKYV 180
D 121 CSTYNRKRGKNGKVSRELSAHTGYLSGCRFLDDNNIVTSSGDTTCALMDIETGQOKYV 180
QY 181 VGHITGDCMSLAIVSPDFNLFTSGACDASAKLMVREGTCROTFTGHESDINATICEFFNGEA 240
D 181 VGHITGDCMSLAIVSPDFNLFTSGACDASAKLMVREGTCROTFTGHESDINATICEFFNGEA 240
QY 241 ICTGSDASCRFLDLRADELICFSEHSIIIGITSVAFLSGLRLFAGYDDFNCAVWDSM 300
D 241 ICTGSDASCRFLDLRADELICFSEHSIIIGITSVAFLSGLRLFAGYDDFNCAVWDSM 300
QY 301 KSERVGLTSGHNDRVSCIGTATACMAVANGSMSEFLAKINN 340
D 301 KSERVGLTSGHNDRVSCIGTATACMAVANGSMSEFLAKINN 340
DB 301 KSERVGLTSGHNDRVSCIGTATACMAVANGSMSEFLAKINN 340

RESULT 5
GBL1_HUMAN STANDARD: PRT; 340 AA.
AC P04901; P04697;
DT 13-AUG-1987 (Rel. 05, created)
DT 13-AUG-1987 (Rel. 05, last sequence update)
DE 15-JUL-1999 (Rel. 38, last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1
GN (TRANSDUCIN BETA CHAIN 1).
OS Homo sapiens (Human), Mus musculus (Mouse), Bos taurus (Bovine), and
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606, 10090, 9913, 9615;
RN 11
RP SEQUENCE FROM N.A.
RC SPECIES-Human; TISSUE-Liver;
RX MEDLINE=87030912; PubMed=3095147;
RA Codina J., Stengel D., Woo S.L.C., Birnbaumer L.;
RT "Beta-subunits of the human liver Gs/Gi signal-transducing proteins
RT and those of bovine retinal rod cell transducin are identical.";
RN 12
FEBS Lett. 207:187-192(1986).
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse; TISSUE-Adrenal gland;
RA Qiu R., Schlimer B.P.;
RN Submitted (JUN-1995) to the EMBL/GenBank/DDIJ databases.
RP SEQUENCE FROM N.A.
RC SPECIES-Bovine;
RX MEDLINE=86177563; PubMed=3083416;
RA Fong H.K.W., Hurley J.B., Hopkins R.S., Mike-Lye R., Johnson M.S.,
RA Doolittle R.F., Simon M.I.;

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RT "Repetitive segmental structure of the transducin beta subunit:
RT homology with the CDC4 gene and identification of related mRNAs.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:2162-2166(1986).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Bovine;
RX MEDLINE=86030675; PubMed=2414128;
RA Sugimoto K., Nukada T., Tanabe T., Takahashi H., Noda M., Minamino N.,
RA Kangawa K., Matsuo H., Hirose T., Inayama S., Numa S.;
RT Primary structure of the beta-subunit of bovine transducin deduced
RT from the cDNA sequence.";
RN FEBS Lett. 191:235-240(1985).
RP [5]
RC SEQUENCE FROM N.A.
RC SPECIES-C. familiaris;
RX MEDLINE=97443667; PubMed=9300552;
RA Kyliana T., Paulin L., Hurwitz M.Y., Hurwitz R.L., Kommonen B.;
RT "Cloning of the cDNA encoding rod photoreceptor
RT cGMP-phosphodiesterase alpha and gamma subunits from the retinal
RT degenerate Labrador retriever dog.";
RN Res. Vet. Sci. 62:293-296(1997).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF HETEROTRIMER.
RX MEDLINE=96107343; PubMed=8521505;
RA Wall M.A., Coleman D.E., Lee E., Iniguez-Lluhi J.A., Posner B.A.,
RA Gilman A.G., Sprang S.R.;
RT "The structure of the G protein heterotrimer Gi alpha 1 beta 1 gamma
RT 2.";
RN Cell 83:1047-1058(1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF BETA-GAMMA DIMER.
RX MEDLINE=96149254; PubMed=8552196;
RA Sondek J., Bohm A., Lambright D.G., Hamm H.E., Sigler P.B.;
RT "Crystal structure of a G-protein beta gamma dimer at 2.1 Å
RT resolution.";
RN Nature 379:369-374(1996).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH PHOSDUCIN.
RX MEDLINE=98416696; PubMed=9739091;
RA Loew A., Ho Y.K., Blundell T., Bax B.;
RT "Phosducin induces a structural change in transducin beta gamma.";
RN Structure 6:1007-1019(1998).
RN [9]
RP -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
RP INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
RP SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
RP GTPASE ACTIVITY. FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
RP EFFECTOR INTERACTION.
RN -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
RN -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
RN -----
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RN -----
RN EMBL; X04526; CAA28207.1; -
RN EMBL; U29055; AAC52805.1; -
RN EMBL; X03073; CAA26875.1; -
RN EMBL; M13236; AAA30792.1; -
RN EMBL; M36430; AAA63265.1; -
RN EMBL; 275134; CAA99446.1; -
RN PIR; A24853; RGHUB1.
RN PIR; A24225; RGHOB1.
RN PDB; 1GG2; 12-FEB-97.
RN PDB; 1GP2; 12-FEB-97.
RN PDB; 1TBB; 01-APR-97.
RN PDB; 1AOR; 16-FEB-99.
RN PDB; 1B9Y; 23-FEB-99.
RN PDB; 1B9Y; 23-FEB-99.
RN MIM; 139380; -

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DR MGD; MGI:95781; Gbhl.
 DR InterPro; IPR001632; -
 DR InterPro; IPR001680; -
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS00682; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family; 3D-structure.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT CONFLICT 71 71 V -> L (IN REF. 4).
 SQ SEQUENCE 340 AA; 37377 MW; 896GBD32D2686598 CRC64;

Query Match 87.2%; Score 1578; DB 1; Length 340;
 Best Local Similarity 83.2%; Pred. No. 3.8e-132;
 Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGEEDQLROAEOLKQIADARKACADVTLAELVSGLEVYGRVOMRTTTLRGLAKIYA 60
 1 MSELQDLROAEOLKQIADARKACADATLSQITNNINPDVGRIOIMRTTTLRGLAKIYA 60
 DB 1 MSELQDLROAEOLKQIADARKACADATLSQITNNINPDVGRIOIMRTTTLRGLAKIYA 60
 QY 61 MHMATSKLLVASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
 61 MHMATSKLLVASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
 DB 61 MHMATSKLLVASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
 QY 121 CSIYNKSRGKRVNYSRELNAHTGYLSCCRFLDDNNIYVSSGDTTCALMDIETGQKTYF 180
 121 CSIYNKSRGKRVNYSRELNAHTGYLSCCRFLDDNNIYVSSGDTTCALMDIETGQKTYF 180
 DB 121 CSIYNKSRGKRVNYSRELNAHTGYLSCCRFLDDNNIYVSSGDTTCALMDIETGQKTYF 180
 QY 181 VGHGTGDCSLVSPDPNFIISGACDASAKIMDVREGTCROFTGHSDDINAIICFPNGEA 240
 181 VGHGTGDCSLVSPDPNFIISGACDASAKIMDVREGTCROFTGHSDDINAIICFPNGEA 240
 DB 181 VGHGTGDCSLVSPDPNFIISGACDASAKIMDVREGTCROFTGHSDDINAIICFPNGEA 240
 QY 241 ICTGSDASCRFLDLRADELICFHSHEIICGITSVAFSLSGRLIFAGYDDFNCAVWDSM 300
 241 ICTGSDASCRFLDLRADELICFHSHEIICGITSVAFSLSGRLIFAGYDDFNCAVWDSM 300
 DB 241 ICTGSDASCRFLDLRADELICFHSHEIICGITSVAFSLSGRLIFAGYDDFNCAVWDSM 300
 QY 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGSMDSFLKIWN 340
 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGSMDSFLKIWN 340
 DB 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGSMDSFLKIWN 340
 301 KADRAGVLAGHNDNRVSCIGVTADGMAVATGSMDSFLKIWN 340

RESULT 6
 GBB1_XENLA STANDARD; PRT; 340 AA.
 ID GBB1_XENLA P79959;
 AC 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 1
 (TRANSDUCIN BETA CHAIN 1) (XGBETA1).
 GN GNB1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OC NCBI_TaxID=8355;
 RN 1;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97109512; Pubmed=8951792;
 RA Devic E., Paquereau L., Rizzotti K., Monier A., Knibiehler B.,
 RA Audigier Y.,
 RT "The mRNA encoding a beta subunit of heterotrimeric GTP-binding
 RT proteins is localized to the animal pole of Xenopus laevis oocyte and
 RT embryos";

RL Mech. Dev. 59:141-151(1996).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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 CC
 DR EMBL; X86969; CAA60532.1; -
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001632; -
 DR InterPro; IPR001680; -
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS00682; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT CONFLICT 71 71 V -> L (IN REF. 4).
 SQ SEQUENCE 340 AA; 37330 MW; DE036FEF60A2D6A9 CRC64;

Query Match 87.0%; Score 1573; DB 1; Length 340;
 Best Local Similarity 82.9%; Pred. No. 1.1e-131;
 Matches 282; Conservative 31; Mismatches 27; Indels 0; Gaps 0;

QY 1 MGEEDQLROAEOLKQIADARKACADVTLAELVSGLEVYGRVOMRTTTLRGLAKIYA 60
 1 MSELQDLROAEOLKQIADARKACADATLSQITNNINPDVGRIOIMRTTTLRGLAKIYA 60
 DB 1 MSELQDLROAEOLKQIADARKACADATLSQITNNINPDVGRIOIMRTTTLRGLAKIYA 60
 QY 61 MHMATSKLLVASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
 61 MHMATSKLLVASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
 DB 61 MHMATSKLLVASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDM 120
 QY 121 CSIYNKSRGKRVNYSRELNAHTGYLSCCRFLDDNNIYVSSGDTTCALMDIETGQKTYF 180
 121 CSIYNKSRGKRVNYSRELNAHTGYLSCCRFLDDNNIYVSSGDTTCALMDIETGQKTYF 180
 DB 121 CSIYNKSRGKRVNYSRELNAHTGYLSCCRFLDDNNIYVSSGDTTCALMDIETGQKTYF 180
 QY 181 VGHGTGDCSLVSPDPNFIISGACDASAKIMDVREGTCROFTGHSDDINAIICFPNGEA 240
 181 VGHGTGDCSLVSPDPNFIISGACDASAKIMDVREGTCROFTGHSDDINAIICFPNGEA 240
 DB 181 VGHGTGDCSLVSPDPNFIISGACDASAKIMDVREGTCROFTGHSDDINAIICFPNGEA 240
 QY 241 ICTGSDASCRFLDLRADELICFHSHEIICGITSVAFSLSGRLIFAGYDDFNCAVWDSM 300
 241 ICTGSDASCRFLDLRADELICFHSHEIICGITSVAFSLSGRLIFAGYDDFNCAVWDSM 300
 DB 241 ICTGSDASCRFLDLRADELICFHSHEIICGITSVAFSLSGRLIFAGYDDFNCAVWDSM 300
 QY 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGSMDSFLKIWN 340
 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGSMDSFLKIWN 340
 DB 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGSMDSFLKIWN 340
 301 KADRAGVLAGHNDNRVSCIGVTADGMAVATGSMDSFLKIWN 340

RESULT 7
 GBB1_RAT STANDARD; PRT; 340 AA.
 ID GBB1_RAT P54311;
 AC 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 1
 (TRANSDUCIN BETA CHAIN 1).
 GN GMBL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Brain;
 RA Kuroda S., Tokunaga C., Konishi H., Kikawa U.;
 RA Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC RECEPTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 DR EMBL: U34958; AACT249.1; -;
 DR HSSP: P04901; ITBG.
 DR InterPro: IPR001632; -;
 DR InterPro: IPR001680; -;
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PROSITE: PS00678; WD_REPEATS_1; 3.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KM Transducer: Repeat; WD repeat: Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA, 37393 MW, 89755AACB2686598 CRC64;

Query Match 86.9%; Score 1572; DB 1; Length 340;
 Best Local Similarity 83.2%; Pred. No. 1.3e-131;
 Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;

QY 1 MGEMQLRDEAEQKQIADAKKACADVTIAELVSGLEVYQVMTTRTLGLHLAKIYA 60
 DB 1 MSRLDRLRDEAEQKQIADAKKACADATLSQITNNIDPVGKMTTRTLGLHLAKIYA 60
 QY 61 MHWATSKLLVSAQSGDKLIVDSYTNVVAIPLRSSVWMTCAVPSNFAVACGLDNM 120
 DB 61 MHWGTDRLVLSAQSOGKLIIDSYTNVVAIPLSSVWMTCAVPSNFAVACGLDNI 120
 QY 121 CSTYLNKSRGNVYKVSRELTAHTGYLSCRCRFDNNIVSSGDTTCALMDITGQOKYTF 180
 DB 121 CSTYLNKTRGNVYKVSRELTAHTGYLSCRCRFDNNIVSSGDTTCALMDITGQOKYTF 180
 QY 181 VGHGTGCMASVDPENFISGACDASAKIMVDPREGTQROTFTGHESDINAIICFPNGEA 240
 DB 181 TGHGTGVMASLAPDRLVFSACDASAKIMVDPREGMKTQTTGHESDINAIICFPNGNA 240
 QY 241 ICTGSDASCRFLDLRADELICFSHESIIICGITSVAESLGRLLFAGYDENCNVWMSM 300
 DB 241 FMTGSDATCRFLDLRADELMTYSHDNIICGITSVSEKSRLLLAGYDENCNVWML 300

QY 301 KSERVILSGHNRVSCIGVTADGMAVATGSMDFELKIN 340
 DB 301 KADRAGDLAGHNRVSCIGVTDDGMAVATGSMDFELKIN 340

RESULT 8
 GMB2_HUMAN
 ID GMB2_HUMAN STANDARD; PRT; 340 AA.
 AC P11016;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 2
 DE (TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT).
 GN GNB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87231903; PubMed=3108879;
 RA Fong H.K.W., Amatruda T.T. III, Birren B.W., Simon M.I.;
 RA "Distinct forms of the beta subunit of GTP-binding regulatory
 RT proteins identified by molecular cloning."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3792-3796(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87317607; PubMed=3114742;
 RA Gao B., Gilman A.G., Robishaw J.D.;
 RA "A second form of the beta subunit of signal-transducing G proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6122-6125(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99018118; PubMed=9799793;
 RA Gloeckner G., Scherer S., Schattevoy R., Boright A., Weber J.,
 RA Tsui L.-C., Rosenthal A.;
 RA "Large-scale sequencing of two regions in human chromosome 7q22:
 RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
 RT reveals 17 genes."
 RL Genome Res. 8:1060-1073(1998).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC RECEPTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M16514; AAA03179.1; -;
 DR EMBL: M16429; AAA63264.1; -;
 DR EMBL: M16538; AAA35922.1; ALT_SEQ.
 DR EMBL: AF053356; AAC8794.1; -;
 DR PIR: B26617; RGHUR2.
 DR HSSP: P04901; ITBG.
 DR MIM: 139390; -;
 DR InterPro: IPR001632; -;
 DR InterPro: IPR001680; -;
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINBPT.
 DR PROSITE: PS00678; WD_REPEATS_1; 3.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.

Transducer; Repeat; WD repeat; Multigene family.

Query Match 84.5%; Score 1528; DB 1; Length 340;
Best Local Similarity 80.9%; Pred. No. 1e-127;
Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

CC 1 MGEMLQROAEQOLKQIADARKACADVTYLAELVSGLEVGRVOMRTTRRLRGLAKIYA 60
CC 1 MSELQOLROAEQOLKQIADARKACGDSLTQITAGIDPVGRIOMRTTRRLRGLAKIYA 60
CC 61 MHWATDSKLVASASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNN 120
CC 61 MHWATDSKLVASASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNN 120
CC 121 CSIYMLKREGNKKVRSRELSAHTGYLSCCRFLDNNITVSSGDTTCALMDIETGQOQTVF 180
CC 121 CSIYMLKREGNKKVRSRELSAHTGYLSCCRFLDNNITVSSGDTTCALMDIETGQOQTVF 180
CC 181 VGHGTDCMSLAVSPDNFLFISGACDASAKLMDVREGTCROTFTGHESDINAIKCFPNCEA 240
CC 181 AGHSGDVMSLSLADPGRTFVSGACDASIKLMDVDSMCROTFTGHESDINAIKCFPNCEA 240
CC 241 ICTGSDASCRFLDRAOELICFHSHTIGITSVAISGLRLLFAGYDDPNCNWDMSM 300
CC 241 FTTSGDSDSCRLFLDRAOELICFHSHTIGITSVAISGLRLLFAGYDDPNCNWDMSM 300
CC 301 KSERVGLSGHNRVSCGLVADGMAVATGSMDSFLKIMN 340
CC 301 KDRAGVLAGHNRVSCGLVADGMAVATGSMDSFLKIMN 340

DB 301 KDRAGVLAGHNRVSCGLVADGMAVATGSMDSFLKIMN 340

RESULT 9
GBB2_MOUSE STANDARD; PRT: 340 AA.

AC P54312:
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 40, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 2
DE (TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT).
GN GNB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6JAPLAN.
RA Kuroda S., Tokunaga C., Konishi H., Kikawa U.;
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE OF 182-297 FROM N.A.
RC STRAIN=C57BL/6JAPLAN.
RA MEDLINE=97011591; Pubmed=8858601;
RA Williams C.J., Schultz R.M., Kopf G.S.;
RT "G protein gene expression during mouse oocyte growth and maturation,
RT and preimplantation embryo development.";
RL Mol. Reprod. Dev. 44:315-323(1996).
CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSDUCER
CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC EFFECTOR INTERACTION.

CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN MEIOGONALLY INCOMPETENT OOCYTES.
CC EXPRESSION INCREASES IN FULLY GROWN MEIOGONALLY INCOMPETENT OOCYTES.
CC EXPRESSION THEN DECREASES DURING METAPHASE-II ARRESTED EGGS. ONE-
CC CELL EMBRIO, TWO-CELL EMBRIO AND EIGHT-CELL EMBRIO STAGES, AND
CC INCREASES AGAIN DURING BLASTOCYST STAGE.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -----
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CC or send an email to license@isb-stb.ch).
CC -----

CC EMBL: U34960; AAC72250.1; -;
CC EMBL: U38505; AAB01736.1; -;
CC HSSP: P04901; 1TBG.
CC MGD: MGI:95784; Gnb2.
CC InterPro: IPR001632; -;
CC InterPro: IPR001680; -;
CC Pfam: PF00400; WD40; 7.
CC PRINTS: PR00319; GPROTEINB.
CC PRINTS: PR00320; GPROTEINBPT.
CC PROSITE: PS00678; WD_REPEATS.1; 3.
CC PROSITE: PS0294; WD_REPEATS.2; 6.
CC PROSITE: PS0294; WD_REPEATS_REGION.1.
CC Transducer; Repeat; WD repeat; Multigene family; Polymorphism.
CC FT REPEAT 53 83 WD 1.
CC FT REPEAT 95 125 WD 2.
CC FT REPEAT 141 170 WD 3.
CC FT REPEAT 182 212 WD 4.
CC FT REPEAT 224 254 WD 5.
CC FT REPEAT 268 298 WD 6.
CC FT REPEAT 310 340 WD 7.
CC FT VARIANT 248 248 S -> A (IN STRAIN CE1).
CC FT SEQUENCE 340 AA; 37333 MM; FECD8AF9B43737D CRC64;

Query Match 84.1%; Score 1521; DB 1; Length 340;
Best Local Similarity 80.3%; Pred. No. 4.2e-127;
Matches 273; Conservative 32; Mismatches 35; Indels 0; Gaps 0;

CC 1 MGEMLQROAEQOLKQIADARKACADVTYLAELVSGLEVGRVOMRTTRRLRGLAKIYA 60
CC 1 MSELQOLROAEQOLKQIADARKACGDSLTQITAGIDPVGRIOMRTTRRLRGLAKIYA 60
CC 61 MHWATDSKLVASASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNN 120
CC 61 MHWATDSKLVASASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNN 120
CC 121 CSIYMLKREGNKKVRSRELSAHTGYLSCCRFLDNNITVSSGDTTCALMDIETGQOQTVF 180
CC 121 CSIYMLKREGNKKVRSRELSAHTGYLSCCRFLDNNITVSSGDTTCALMDIETGQOQTVF 180
CC 181 VGHGTDCMSLAVSPDNFLFISGACDASAKLMDVREGTCROTFTGHESDINAIKCFPNCEA 240
CC 181 AGHSGDVMSLSLADPGRTFVSGACDASIKLMDVDSMCROTFTGHESDINAIKCFPNCEA 240
CC 241 ICTGSDASCRFLDRAOELICFHSHTIGITSVAISGLRLLFAGYDDPNCNWDMSM 300
CC 241 FTTSGDSDSCRLFLDRAOELICFHSHTIGITSVAISGLRLLFAGYDDPNCNWDMSM 300
CC 301 KSERVGLSGHNRVSCGLVADGMAVATGSMDSFLKIMN 340
CC 301 KDRAGVLAGHNRVSCGLVADGMAVATGSMDSFLKIMN 340

DB 301 KDRAGVLAGHNRVSCGLVADGMAVATGSMDSFLKIMN 340

RESULT 10
GBB1_CAEL STANDARD; PRT: 340 AA.

AC P17343; Q19394;

Query Match 82.9%; Score 1500; DB 1; Length 340;
 Best Local Similarity 79.4%; Pred. No. 3e-125;
 Matches 270; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

QY 1 MGEMLROAEQOLKQADARACADVTLAELVSGLEVGVROMTTRTIRGLAKIYA 60
 DB 1 MSELQLOAEQOLKQADARACADVTLAELVSGLEVGVROMTTRTIRGLAKIYA 60
 QY 61 MHWATSKLLVASADQGLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 DB 61 MHWATSKLLVASADQGLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 QY 121 CSYLNKSGREGVAVRSKRLPGHTGTLSCRFDDNQIITSSGDTTCALMDIETGQKTF 180
 DB 121 CSYLNKSGREGVAVRSKRLPGHTGTLSCRFDDNQIITSSGDTTCALMDIETGQKTF 180
 QY 181 VGHGTDCMSLAVSPDFNFISGACDASAKLMDVREGTCRQTFTHGSHDINACEFNGEA 240
 DB 181 AGHSGDVMSLSPDGRFVSGACDASAKLMDVREGTCRQTFTHGSHDINACEFNGEA 240
 QY 241 ICTGSDASCRFLDLRADQELICSHESIICGITSVAFLSGLIFAGYDDPNCNWDNM 300
 DB 241 FTTGSDATCRFLDLRADQELIYSHDNIICGITSVAFLSGLIFAGYDDPNCNWDNM 300
 QY 301 KSERVGIISGHDRVSCGLVTDGMAVATGSMDSFLKTN 340
 DB 301 KGRSGVLAGHNRVSCGLVTDGMAVATGSMDSFLKTN 340

RESULT 12

GBB4_MOUSE STANDARD: PRT: 340 AA.

AC P29387;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).
 GN GNB4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92181467; PubMed=1543505;
 RA von Weizsäcker E., Strathmann M.P., Simon M.I.;
 RT "Diversity among the beta subunits of heterotrimeric GTP-binding proteins: characterization of a novel beta-subunit cDNA."
 RL Biochem. Biophys. Res. Commun. 183:350-356(1992).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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 CC -----
 CC EMBL: S86124; AAB21609.1; -
 CC EMBL: M87286; AAA37756.1; -
 CC EMBL: M63658; AAA37664.1; -
 CC PIR: J50659; GMSB4.
 CC HSP: P04901; ITBG.

DR MGI:104581; Gnb4.
 DR InterPro: IPR001632; -
 DR InterPro: IPR001680; -
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINB.
 DR PROSITE: PS00678; WD_REPEATS_1; 3.
 DR PROSITE: PS00682; WD_REPEATS_2; 6.
 DR PROSITE: PS0294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37354 MW; B2IEB29BA862B1E CRC64;

Query Match 82.9%; Score 1500; DB 1; Length 340;
 Best Local Similarity 78.8%; Pred. No. 3e-125;
 Matches 268; Conservative 38; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGEMLROAEQOLKQADARACADVTLAELVSGLEVGVROMTTRTIRGLAKIYA 60
 DB 1 MSELQLOAEQOLKQADARACADVTLAELVSGLEVGVROMTTRTIRGLAKIYA 60
 QY 61 MHWATSKLLVASADQGLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 DB 61 MHWATSKLLVASADQGLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 QY 121 CSYLNKSGREGVAVRSKRLPGHTGTLSCRFDDNQIITSSGDTTCALMDIETGQKTF 180
 DB 121 CSYLNKSGREGVAVRSKRLPGHTGTLSCRFDDNQIITSSGDTTCALMDIETGQKTF 180
 QY 181 VGHGTDCMSLAVSPDFNFISGACDASAKLMDVREGTCRQTFTHGSHDINACEFNGEA 240
 DB 181 TGHSGDVMSLSPDGRFVSGACDASAKLMDVREGTCRQTFTHGSHDINACEFNGEA 240
 QY 241 ICTGSDASCRFLDLRADQELICSHESIICGITSVAFLSGLIFAGYDDPNCNWDNM 300
 DB 241 FATSDDATCRFLDLRADQELIYSHDNIICGITSVAFLSGLIFAGYDDPNCNWDNM 300
 QY 301 KSERVGIISGHDRVSCGLVTDGMAVATGSMDSFLKTN 340
 DB 301 KGRSGVLAGHNRVSCGLVTDGMAVATGSMDSFLKTN 340

RESULT 13

GBB_LYMST STANDARD: PRT: 341 AA.

AC Q08706;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.
 OS Lymnaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Lymnaea.
 OX NCBI_TaxId=6523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CNS;
 RX MEDLINE=94242793; PubMed=7514444;
 RA Knol J.C., Roovers E., van Kesteren E.R., Planta R.J.,
 RA Vreugdenhil R., van Heerikhuizen H.;
 RT "A G-protein beta subunit that is expressed in the central nervous system of the mollusc Lymnaea stagnalis is identified through cDNA cloning".
 RL Biochim. Biophys. Acta 1222:129-133(1994).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE

CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC EFFECTOR INTERACTION.
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Z23105; CAAB0652.1; -
CC HSSP: P04901; 1GP2.
CC InterPro: IPR001632; -
CC InterPro: IPR001680; -
CC Pfam: PF00400; WD40; 7.
CC PRINTS: PR00319; GPROTEINB.
CC PRINTS: PR00320; GPROTEINBPT.
CC PROSITE: PS00678; WD_REPEATS_1; 2.
CC PROSITE: PS50082; WD_REPEATS_2; 5.
CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
CC Transducer: Repeat; WD repeat.
CC FT REPEAT 54 84 WD 1.
CC FT REPEAT 96 126 WD 2.
CC FT REPEAT 142 171 WD 3.
CC FT REPEAT 183 213 WD 4.
CC FT REPEAT 225 253 WD 5.
CC FT REPEAT 268 298 WD 6.
CC FT REPEAT 311 341 WD 7.
CC
CC SEQUENCE 341 AA; 37320 MW; 4A262588387592E CRC64;

Query Match 81.8%; Score 1480; DB 1; Length 341;
Best Local Similarity 79.6%; Pred. No. 1,8e-123;
Matches 269; Conservative 30; Mismatches 39; Indels 0; Gaps 0;

QY 3 EMBLROEAEOLKQADARKACADYTLAEVSGLEVGVGMQRTTRTGRHLAKIYAM 62
DB 4 DLEALROETBOLKQAEARKKAGDITLQACSGVEVGIQRTTRTGRHLAKIYAM 63
QY 63 WATDSKLLVASODGKLIWDSYTNKVAHPIPLRSSVWMTCAAPSGNFVACGGLDNMS 122
DB 64 WATDSKLLVASODGKLIWDSYTNKVAHPIPLRSSVWMTCAAPSGNFVACGGLDNMS 123
QY 123 IYNLKSREGVAVKYSRELTAHTGLSCRFIDNNIYTSAGDTTCALMDIETGQOKTVEG 182
DB 124 IYSLKTRREGVAVKYSRELTAHTGLSCRFIDNNIYTSAGDTTCALMDIETGQOKTVEG 183
QY 183 HTGCGMSLAVSPDFNLTISGACDASAKLMDVREGTCRQTFTHESDINATCFPNGEATC 242
DB 184 HTGCGMSLAVSPDFNLTISGACDASAKLMDVREGTCRQTFTHESDINATCFPNGEATC 243
QY 243 TGSDDASCRFLDRADELICFHSHESTIGITVAFSLGRLLFAGYDDPFCNVWDSMS 302
DB 244 TGSDDATCRFLDRADELICFHSHESTIGITVAFSLGRLLFAGYDDPFCNVWDSMS 303
QY 303 ERVGIISGHDNRVSCIGVYADGNAVATGSDSTLKTWN 340
DB 304 ETHGVLAGHDNRVSCIGVYADGNAVATGSDSTLKTWN 341
RESULT 14
ID GBLI_HOMAM STANDARD: PRT; 340 AA.
AC 045040;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(11)/G(5)/G(7) BETA SUBUNIT 1
(TRANSDUCIN BETA CHAIN 1).

GN GBLTAL.
OS Homarus americanus (American lobster).
OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_Taxid=6706;
RN (1)
RP SEQUENCE FROM N.A. PubMed-9740024;
RA MEDLINE=98410740; Lander T.M., McClintock T.S.;
RX Xu F., Hollins B., Landers T.M., McClintock T.S.;
RT "Molecular cloning of a lobster Gbeta subunit and Gbeta expression in
RT olfactory receptor neuron dendrites and brain neuropil."
RL J. Neurobiol. 36:525-536(1998).
CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC EFFECTOR INTERACTION.
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF044735; AAC02998.1; -
CC InterPro: IPR001632; -
CC InterPro: IPR001680; -
CC Pfam: PF00400; WD40; 7.
CC PRINTS: PR00319; GPROTEINB.
CC PRINTS: PR00320; GPROTEINBPT.
CC PROSITE: PS00678; WD_REPEATS_1; 3.
CC PROSITE: PS50082; WD_REPEATS_2; 6.
CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
CC Transducer: Repeat; WD repeat; Multigene family.
CC FT REPEAT 53 83 WD 1.
CC FT REPEAT 95 125 WD 2.
CC FT REPEAT 141 170 WD 3.
CC FT REPEAT 182 212 WD 4.
CC FT REPEAT 224 254 WD 5.
CC FT REPEAT 268 298 WD 6.
CC FT REPEAT 310 340 WD 7.
CC
CC SEQUENCE 340 AA; 37409 MW; 3483245F9291D82E CRC64;

Query Match 81.8%; Score 1479; DB 1; Length 340;
Best Local Similarity 78.2%; Pred. No. 2,1e-123;
Matches 266; Conservative 35; Mismatches 39; Indels 0; Gaps 0;

QY 1 MCEMDLOEAEOLKQADARKACADYTLAEVSGLEVGVGMQRTTRTGRHLAKIYA 60
DB 1 MCEMDLOEAEOLKQADARKACADYTLAEVSGLEVGVGMQRTTRTGRHLAKIYA 60
QY 61 MHWANDSKLLVASODGKLIWDSYTNKVAHPIPLRSSVWMTCAAPSGNFVACGGLDNM 120
DB 61 MHWANDSKLLVASODGKLIWDSYTNKVAHPIPLRSSVWMTCAAPSGNFVACGGLDNM 120
QY 121 CSYINLKSREGVAVKYSRELTAHTGLSCRFIDNNIYTSAGDTTCALMDIETGQOKTVE 180
DB 121 CSYINLKSREGVAVKYSRELTAHTGLSCRFIDNNIYTSAGDTTCALMDIETGQOKTVE 180
QY 181 VGHTEGDCMSLAVSPDFNLTISGACDASAKLMDVREGTCRQTFTHESDINATCFPNGEA 240
DB 181 VGHTEGDCMSLAVSPDFNLTISGACDASAKLMDVREGTCRQTFTHESDINATCFPNGEA 240
QY 241 TGTGTDVMSLSPDMRTFTSGACDASAKLMDVREGTCRQTFTHESDINATCFPNGEA 300
DB 241 TGTGTDVMSLSPDMRTFTSGACDASAKLMDVREGTCRQTFTHESDINATCFPNGEA 300

QY 301 KSERVGLSGHNDNRVSCGLVADGMAVATGSMDSFSLKTN 340
DB 301 RTERAGVLAGHNDNRVSCGLVTEGDMANVATGSMDSFSLKTN 340

RESULT 15

ID GBB2_BOVIN STANDARD; PRT; 326 AA.

AC P11017;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 2
GN (TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

RP [1]
RN SEQUENCE FROM N.A.
RA MEDLINE=87231903; PubMed=3108879;
RX Fong H.K.W., Amatruda T.T. III, Birren B.W., Simon M.L.;
RT "Distinct forms of the beta subunit of GTP-binding regulatory
RL proteins identified by molecular cloning.";
Proc. Natl. Acad. Sci. U.S.A. 84:3792-3796(1987).
[2]
RN SEQUENCE OF 88-302 FROM N.A.
RX MEDLINE=87317607; PubMed=3114742;
RA Gao B., Gilman A.G., Robishaw J.D.;
RT "A second form of the beta subunit of signal-transducing G proteins.";
Proc. Natl. Acad. Sci. U.S.A. 84:6122-6125(1987).

CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC RECEPTOR INTERACTION.
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- SIMILARITY: CONSTRAINTS 7 WD REPEATS (TRP-ASP DOMAINS).

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CC or send an email to license@isb-sib.ch).

DR EMBL: M16480; AAA30553.1; -;
DR EMBL: M36431; AAA62717.1; -;
DR EMBL: M16539; AAA30552.1; -;
DR PIR: A26617; RGH082.
DR HSSP: P04901; 1GP2.
DR InterPro: IPR001680; -;
DR Pfam: PF00400; WD40; 7.
DR PROSITE: PS00678; WD_REPEATS_1; 3.
DR PROSITE: PS50082; WD_REPEATS_2; 6.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Transducer; Repeat; WD repeat; Multigene family.

FT NON_TER 1 1
FT REPEAT 39 69 WD 1.
FT REPEAT 81 111 WD 2.
FT REPEAT 127 136 WD 3.
FT REPEAT 168 198 WD 4.
FT REPEAT 210 240 WD 5.
FT REPEAT 254 284 WD 6.
FT REPEAT 296 326 WD 7.
FT CONFLICT 271 271 L -> V (IN REF. 2).
SQ SEQUENCE 326 AA; 35645 MW; EE9B0EF5BCC51R23 CRC64;

Query Match 81.2%; Score 1469; DB 1; Length 326;

Best Local Similarity 80.7%. Pred. No. 1,6e-122;
Matches 263; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 15 KKOIADARKACADVTLAELVSGLEVGVGRVOMRTTRTLRGHIAKIYAMWATDSKLVSAS 74
DB 1 RNQIRDARKACDSTLTQTITAGLDPVGRIOHRTTRTLRGHIAKIYAMWATDSKLVSAS 60
QY 75 QDGKLIWDSYTTNKVHAIPLRSSWVMTCAVAPSGNFVACGGLDMCSYIMLKSGREGNVK 134
DB 61 QDGKLIWDSYTTNKVHAIPLRSSWVMTCAVAPSGNFVACGGLDMCSYIMLKSGREGNVK 120
QY 135 VSRELSAHTGYLSCCRFLDDNNIVTSVSGDTTCALMDIETGQOKVFPVGHTRDCLAVSP 194
DB 121 VSRELSAHTGYLSCCRFLDDNNIVTSVSGDTTCALMDIETGQOKVFPVGHTRDCLAVSP 180
QY 195 DNFELISACDASAKLMDVREGTCRQFTGTHESDINAICFPNGEALCTGSDASCRLFD 254
DB 181 DGRFVSGACDASIKLMDVREGTCRQFTGTHESDINAICFPNGEALCTGSDASCRLFD 240
QY 255 LRADQLICFHSHESTICITVAFSLSGRLFPAGYDPCNVWDSKRSERYGLISGHNR 314
DB 241 LRADQLICFHSHESTICITVAFSLSGRLFPAGYDPCNVWDSKRSERYGLISGHNR 300
QY 315 VSCLGVTADGMAVATGSMDSFSLKTN 340
DB 301 VSCLGVTADGMAVATGSMDSFSLKTN 326

Search completed: September 28, 2001, 10:34:29
Job time: 284 sec

Fri Sep 28 10:45:15 2001

us-09-492-029-5.rsp

Page 12

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: September 28, 2001, 10:34:06 ; Search time 38.04 Seconds
(without alignments)
1182.537 Million cell updates/second

```

Title: US-09-492-029-5
Perfect score: 1809
Sequence: 1 MGEWDLRQEALEQLKQLAD.....TADGNAVATGSDSFLKIWN 340

```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425020
```

```

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

```

Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

```
Database :
    sp archaea:*
    1: sp archaea:*
    2: sp bacteria:*
    3: sp fungi:*
    4: sp human:*
    5: sp invertebrate:*
    6: sp mammal:*
    7: sp rhc:*
    8: sp organelle:*
    9: sp phage:*
    10: sp plant:*
    11: sp rodent:*
    12: sp unclassified:*
    13: sp vertebrate:*
    14: sp virus:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1670	92.3	340	13	09DFG9	09dfg9 ambystoma t
2	1575	87.1	340	13	09DFH0	09dfh0 ambystoma t
3	1563	86.4	340	11	09QWG8	09qwg8 rattus norv
4	1516	83.8	340	41	09HAY0	09hay0 homo sapien
4	1503	83.1	340	11	09JHX8	09jhx8 mus muscul
6	1252	69.2	352	3	093887	093887 cryptococcu
5	1226.5	67.8	347	3	09HFS3	09hfs3 pneumocysti
7	1219.5	67.4	352	3	074214	074214 emeritella
8	967.5	53.5	358	4	09WJ31	09wj31 drosophila
9	949.5	52.5	395	5	09HAB9	09hab9 homo sapien
10	831	45.9	346	4	09NEZ1	09nez1 calliphora
11	820.5	45.4	377	10	09XFK0	09xfk0 pisum sativi
12	819	45.3	377	10	09SW94	09sw94 pisum sativi
13	814	45.0	346	5	09YW29	09yw29 drosophila
14	809	44.7	377	10	09FEV61	09fev61 nicotiana
15	794	43.9	380	10	064944	064944 aenea fatu
16	743.5	41.1	380	4	09UFG3	09ufg3 homo sapien
17	689.5	36.1	426	3	09Y758	09y7b8 kluyveromye
18	584	37.8	186	5	045041	045041 homarus ame

20	635	35.1	371	5	Q9X2V6	Q9XV6	geodia	cydo
21	609	33.7	123	11	061621	Q61621	mus	musculi
22	585.5	32.4	240	10	040456	Q40456	nicotiana	t
23	317	17.5	1241	2	Q9XBDB	Q9XBDB	amycolatis	
24	308	17.0	333	10	Q9SY00	Q9SY00	arabidopsi	
25	305.5	16.9	502	3	074855	074855	schizosacch	
26	304	16.8	522	4	043445	043445	homo sapien	
27	303	16.7	579	5	076734	076734	dictyosteli	
28	300.5	16.6	485	4	Q9NVX2	Q9NVX2	homo sapien	
29	300.5	16.6	551	3	014432	014432	schizosacch	
30	300.5	16.6	386	3	Q9YUG8	Q9YUG8	schizosacch	
31	300	16.6	520	4	042864	043864	homo sapien	
32	299	16.5	1049	2	Q9ZEM4	Q9ZEM4	streptomyces	
33	299	16.5	1676	2	Q9XKX9	Q9XKX9	streptomyces	
34	296	16.4	521	4	043172	043172	homo sapien	
35	295.5	16.3	318	5	Q96653	Q96653	trypansom	
36	294.5	16.3	317	13	Q96W71	Q96W71	xenopus la	
37	294	16.3	334	4	Q9NM77	Q9NM77	homo sapien	
38	292	16.1	473	10	Q9FLX9	Q9FLX9	arabidopsi	
39	287	15.9	587	5	044083	044083	caenorhabdit	
40	284.5	15.7	476	13	Q93531	Q93531	xenopus la	
41	283.5	15.7	481	5	Q9VPR4	Q9VPR4	drosophila	
42	282	15.6	313	5	Q9UUY2	Q9UUY2	euprymna sc	
43	281.5	15.6	330	4	Q9NUD4	Q9NUD4	homo sapien	
44	280	15.5	553	5	Q9VV10	Q9VV10	drosophila	
45	279.5	15.5	480	5	Q96995	Q96995	drosophila	

ALIGNMENTS

RESULT	1
Q9DFG9	
ID	Q9DFG9
AC	Q9DFG9; PRELIMINARY; PRT; 340 AA.
DT	01-MAR-2001 (TEMBIrel, 16, Created)
DT	01-MAR-2001 (TEMBIrel, 16, Last sequence update)
DT	01-MAR-2001 (TEMBIrel, 16, Last annotation update)
DT	G-PROTEIN B3 SUBUNIT.
DE	Amystroma tigrinum (Tiger salamander).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Ampibilia; Batrachia; Caudata; Salamandroides; Amylostomidae;
OC	Ambystoma.
OX	NCBI_TaxID=8305;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=RETINA;
RA	Ryan J.C., Crouch R.K., Ma J.;
RT	"Cloning and Characterization of G-protein Beta subunits from the
RT	Salamander Retina.";
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
SR	EMBL: AF277162; AAC31061.1; -
SQ	SEQUENCE 340 AA; 3735 MW; 6C284C100552DBE CRC64;

[illegible]

Db 181 MGTGDCMSLAVSPDFRIFVSGACDATTAKINDRECTGRTFTGHESDINAIICFPNGEA 240
 QY 241 ICTGSDASCRFLDLADDELICFSHESITIGITSVAFLSGRLIFAGYDPCNVWDSM 300
 Db 241 VCTGSDASCRFLDLADDELICFSHESITIGITSVAFLSGRLIFAGYDPCNVWDSM 300
 QY 301 KSERVGLISGHDNRVSCGLVTADGMAVATGSDSFLKTN 340
 Db 301 KSERVGLISGHDNRVSCGLVTADGMAVATGSDSFLKTN 340

RESULT 2
 Q9DFH0 PRELIMINARY; PRT; 340 AA.
 AC Q9DFH0: (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE G-PROTEIN B1 SUBUNIT.
 OS Ambystoma tigrinum (tiger salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;
 OX NCBI_TaxID=8305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=RETINA;
 RA Ryan J.C., Crouch R.K., Ma J.,
 RT "Cloning and Characterization of G-protein Beta subunits from the
 RL Salamander Retina."
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF271761; AAG31060.1; -
 SO SEQUENCE 340 AA; 37332 MW; 84E1451FDD83D8F3 CRC64;

Query Match 87.1%; Score 1575; DB 13; Length 340;
 Best Local Similarity 82.9%; Pred. No. 3.9e-139;
 Matches 282; Conservative 31; Mismatches 27; Indels 0; Gaps 0;

QY 1 MGEMDLROEAEOLKQIADARKACADYLAELVSGLEVGRVOMRTTRTLRGLAKIYA 60
 Db 1 MSELQDLROEAEOLKQIADARKACADYLAELVSGLEVGRVOMRTTRTLRGLAKIYA 60
 QY 61 MHATDLSKLVSASODGKLIYWDSTYTNKVAIPLRSSWMTCAAPSGNEVACGGIDNI 120
 Db 61 MHATDLSKLVSASODGKLIYWDSTYTNKVAIPLRSSWMTCAAPSGNEVACGGIDNI 120
 QY 121 CSITNLSKREGNVAVSRELTAHTGYLSCRFDDNNIYVSSGDTTCALMDIETGQKTFV 180
 Db 121 CSITNLSKREGNVAVSRELTAHTGYLSCRFDDNNIYVSSGDTTCALMDIETGQKTFV 180
 QY 181 VGHGTDCMSLAVSPDFRIFVSGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
 Db 181 VGHGTDCMSLAVSPDFRIFVSGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
 QY 241 ICTGSDASCRFLDLADDELICFSHESITIGITSVAFLSGRLIFAGYDPCNVWDSM 300
 Db 241 ICTGSDASCRFLDLADDELICFSHESITIGITSVAFLSGRLIFAGYDPCNVWDSM 300
 QY 301 KSERVGLISGHDNRVSCGLVTADGMAVATGSDSFLKTN 340
 Db 301 KSERVGLISGHDNRVSCGLVTADGMAVATGSDSFLKTN 340
 QY 301 KADRAVGLAGHDNRVSCGLVTADGMAVATGSDSFLKTN 340
 Db 301 KADRAVGLAGHDNRVSCGLVTADGMAVATGSDSFLKTN 340

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Wang X.B., Funada M., Imai Y., Revey R.S., Ujike H., Vandenbergh D.J.,
 RA Uhl G.R.;
 RT "Fdb1: A psychostimulant-regulated gene essential for establishing
 RT cocaine sensitization."
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U88324; AAD00650.1; -
 DR HSSP: P04901; 1TBC.
 DR InterPro: IPR001632; -
 DR InterPro: IPR001680; -
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINBPT.
 DR PROSITE: PS00678; WD_REPEATS; UNKNOWN_3.
 DR SMART: SM00320; WD40; 1.
 KW Repeat: WD repeat.
 SO SEQUENCE 340 AA; 37387 MW; D9EBEC6B0FF7EC57 CRC64;

Query Match 86.4%; Score 1563; DB 11; Length 340;
 Best Local Similarity 82.4%; Pred. No. 5.1e-138;
 Matches 280; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

QY 1 MGEMDLROEAEOLKQIADARKACADYLAELVSGLEVGRVOMRTTRTLRGLAKIYA 60
 Db 1 MSELQDLROEAEOLKQIADARKACADYLAELVSGLEVGRVOMRTTRTLRGLAKIYA 60
 QY 61 MHATDLSKLVSASODGKLIYWDSTYTNKVAIPLRSSWMTCAAPSGNEVACGGIDNI 120
 Db 61 MHATDLSKLVSASODGKLIYWDSTYTNKVAIPLRSSWMTCAAPSGNEVACGGIDNI 120
 QY 121 CSITNLSKREGNVAVSRELTAHTGYLSCRFDDNNIYVSSGDTTCALMDIETGQKTFV 180
 Db 121 CSITNLSKREGNVAVSRELTAHTGYLSCRFDDNNIYVSSGDTTCALMDIETGQKTFV 180
 QY 181 VGHGTDCMSLAVSPDFRIFVSGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
 Db 181 VGHGTDCMSLAVSPDFRIFVSGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
 QY 241 ICTGSDASCRFLDLADDELICFSHESITIGITSVAFLSGRLIFAGYDPCNVWDSM 300
 Db 241 ICTGSDASCRFLDLADDELICFSHESITIGITSVAFLSGRLIFAGYDPCNVWDSM 300
 QY 301 KSERVGLISGHDNRVSCGLVTADGMAVATGSDSFLKTN 340
 Db 301 KSERVGLISGHDNRVSCGLVTADGMAVATGSDSFLKTN 340
 QY 301 KADRAVGLAGHDNRVSCGLVTADGMAVATGSDSFLKTN 340
 Db 301 KADRAVGLAGHDNRVSCGLVTADGMAVATGSDSFLKTN 340

RESULT 4
 Q9HAY0 PRELIMINARY; PRT; 340 AA.
 AC Q9HAY0: (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT 4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
 RT "Cloning and Characterization of Human G-protein Beta 4."
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF300648; AAG18442.1; -

Db 252 AFATGSDSDACKFLDLRADRELNSAHDNITLCITSVAFSISGRVLFAGYDYNQNCVMDT 311
 QY 300 MKSERGILSGHNRVSCGLVADGMAVATGSDMSFLKIWN 340
 Db 312 LKGERIGVLGHENRVSCMGVSGDVALCTGSDMSDLKIVMS 352

RESULT 7
 Q9HFS3 PRELIMINARY: PRT: 347 AA.

AC 09HFS3
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN, BETA SUBUNIT.
 OS Pneumocystis carinii.
 OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
 NCBI_TaxID=4754;
 RX NCBL_TaxID=4754;
 RP SEQUENCE FROM N.A.
 RA Puri V., Park J.G., Limper A.H., Thomas C.F. Jr.;
 RT "The Pneumocystis carinii guanine nucleotide-binding protein beta
 subunit."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF036565; AAC27720.1;
 SQ SEQUENCE 347 AA; 38438 MW; FEE1495006E24882 CRC64;

Query Match 67.8%; Score 1226.5; DB 3; Length 347;
 Best Local Similarity 66.9%; Pred. No. 1.5e-106;
 Matches 222; Conservative 47; Mismatches 62; Indels 1; Gaps 1;

QY 9 QEADQLKQIADARKACADVTIAELVSGLEVYGVQMRRTTGLHAKIYAMHATDSK 68
 Db 15 KEAEVLEKIKKKDELADNLNRMATLDVIERLSIRVATYTLKGHLAKIYAMHSTDK 74
 QY 69 LLVASADGKLIWSDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNMCSIYNLKS 128
 Db 75 HLVASADGKLIWSDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNMCSIYNLKS 134
 QY 129 REGNVKYSRELSAHTGYLSCRFIDNNIYSSGDTTCALMDIETGQKTVVGHGTGDM 188
 Db 135 KDGAKIARELMATHTGLSCRFIDNNIYSSGDTTCALMDIETGQKTVVGHGTGDM 194
 QY 189 SLAVSP-DFNLFTSGACDASAKLMDVREGTCROTFTGHESDINATCFPPNGEATCGSD 247
 Db 195 SLSTHPTNPMFLFVSGACDAFAKIMDIRIGSVQTFAGHESDINATCFPPNGEATCGSD 254
 QY 248 ASCEPLRLADDELICFHSHTICGITSVAFLSGLRLEFAGYDDFNQVWDSMKSERVGI 307
 Db 255 ASCEPLRLADDELICFHSHTICGITSVAFLSGLRLEFAGYDDFNQVWDSMKSERVGI 314
 QY 308 LSGHNRVSCGLVADGMAVATGSDMSFLKIWN 339
 Db 315 LSGHNRVSCGLVADGMAVATGSDMSFLKIWN 346

RESULT 8
 Q74214 PRELIMINARY: PRT: 352 AA.
 AC 074214
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DE G-PROTEIN BETA SUBUNIT.
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 NCBI_TaxID=5072;
 RX NCBL_TaxID=5072;

RP SEQUENCE FROM N.A.
 RA Rosen S., Yu J.-H., Adams T.H.;
 RT "Aspergillus nidulans fiba suppressor gfad identifies the G-beta
 subunit of a heterotrimeric G protein."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF036182; AAC33436.1;
 DR HSSP; P04901; 1TBG.
 DR InterPro; IPR001632;
 DR InterPro; IPR001680;
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.
 DR SMART; SM00320; WD40; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 352 AA; 38888 MW; 186A16886BADFA66 CRC64;

Query Match 67.4%; Score 1219.5; DB 3; Length 352;
 Best Local Similarity 64.6%; Pred. No. 6.9e-106;
 Matches 223; Conservative 50; Mismatches 65; Indels 7; Gaps 3;

QY 2 GEMEQ-----LROEADQLKQIADARKACADVTIAELVSGLEVYGVQMRRTTGLH 55
 Db 6 GEMEQ-----LROEADQLKQIADARKACADVTIAELVSGLEVYGVQMRRTTGLH 55
 QY 56 AKIYAMHATDSKLIWSDYTTNKVHAIPLRSSWMTCAVAPSGNFVACG 115
 Db 66 AKIYAMHATDSKLIWSDYTTNKVHAIPLRSSWMTCAVAPSGNFVACG 125
 QY 116 GLDNMCSIYNLKSREGNVKYSRELSAHTGYLSCRFIDNNIYSSGDTTCALMDIETGQ 175
 Db 126 GLDNMCSIYNLKSREGNVKYSRELSAHTGYLSCRFIDNNIYSSGDTTCALMDIETGQ 185
 QY 176 QKTVFVGHGTGDMSLAVSP-DFNLFTSGACDASAKLMDVREGTCROTFTGHESDINATCF 234
 Db 186 KTVFVGHGTGDMSLAVSP-DFNLFTSGACDASAKLMDVREGTCROTFTGHESDINATCF 245
 QY 235 FPNGEALCTGSDASCEPLRLADDELICFHSHTICGITSVAFLSGLRLEFAGYDDFNQ 294
 Db 246 FPNGEALCTGSDASCEPLRLADDELICFHSHTICGITSVAFLSGLRLEFAGYDDFNQ 305
 QY 295 NVWDSMKSERGILSGHNRVSCGLVADGMAVATGSDMSFLKIWN 339
 Db 306 NVWDSMKSERGILSGHNRVSCGLVADGMAVATGSDMSFLKIWN 350

RESULT 9
 Q9W3J1 PRELIMINARY: PRT: 358 AA.
 AC 09W3J1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE CG10763 PROTEIN.
 GN CG10763.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RX NCBL_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RA STRAIN-BERKELEY;
 RC MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Abmayr A., An H.-J., Andrews-Plambeck C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu T., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck H., Brokstein P., Brottier P.,
 RA Burtis K.C., Busan D.A., Butler K., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 RA de Padlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dopp L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laspo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mervlov G., Mishina N.V., Mobarry C., Morris J., Mostreli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relneert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Stapleton M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhan G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003443; AAF46336.1; -.
 DR HSP: P04901; 1786.
 DR FLYBASE: FBgn0030011; CG10763.
 DR InterPro: IPR001632; -.
 DR InterPro: IPR001632; -.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINB.
 DR PROSITE: PS00678; WD-REPEATS; 3.
 DR SMART: SM00320; WD40; 1.
 DR Repeat: WD repeat.
 SO SEQUENCE 358 AA; 39354 MW; E9C6DEF91C503231 CRC64;

Query Match 53.5%; Score 967.5; DB 5; Length 358;
 Best Local Similarity 50.0%; Pred. No. 2.5e-82;
 Matches 170; Conservative 78; Mismatches 89; Indels 3; Gaps 2;

QY 3 EMBL:AE003443:K01ADARKACADVTAAELVSGLEEVGRVOMTRRLRGLAKIYAMH 62
 DB 18 KASLVREAEINKTKLEERKLNVDNLSNIAERLQIAYVNIKPKYKLGHOAKVLCCTD 77
 QY 63 WATDSKLVSASODKRLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGIDNNCS 122
 DB 78 WSPDKRHITSSQDQRLIITWDFTTNKEHAYMPTTWMACAYAPSGNFVACGGIDNNCS 137
 QY 123 IYNKSRBEGNVKVSSELSAHTGYLSCCRFLD-DNNITVSSGDTTCALMDITGQOKTYP 181
 DB 138 YPITSDEMAAKKRTVGHHSYMSCIYPNSDQILITFGSGDTTCALMDVSGQLQSFH 197
 QY 182 GHTGCMCLAVSPD--FNLFTSGACDASAKLMDVREGRCROFTGHEDINACIFPPNGE 239
 DB 198 GHSIGVYMDLAPNETGTFTFVSGSDRMATFWDKMSGVHVOVSFEHDSVSKRHPGCD 257
 QY 240 AICTGSDASCRFLDLRADDELICFSHESIIGITVSFSLSGRLIFAGYDFKNCVWDS 299
 DB 258 AIATGSDSSCRLLYDMRADREVAIVFAKESITIFGVNSVDFSVSGRLIFAGYDYNLMDT 317
 QY 300 MKSERVGLISGHDNRVSLGVTADGMAVATGSDSFLKIWM 339
 DB 318 LKSERVGLISGHDNRVSLGVTADGMAVATGSDSFLKIWM 357

RESULT 10
 Q9HAY9 ID Q9HAY9 PRELIMINARY; PRT; 395 AA.
 AC Q9HAY9;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT 5L.
 GN GNB5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pohl H.L. III, Ikeda S.R., Aronstam R.S.;
 RT "Cloning and characterization of human G-protein beta 5L subunit."
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF30650; AAC18444.1; -.
 SO SEQUENCE 395 AA; 43566 MW; E001B07FCFA587AD CRC64;

Query Match 52.5%; Score 949.5; DB 4; Length 395;
 Best Local Similarity 52.2%; Pred. No. 1.4e-80;
 Matches 178; Conservative 56; Mismatches 102; Indels 5; Gaps 3;

QY 4 EMBL:AE003443:K01ADARKACADVTAAELVSGLEEVGRVOMTRRLRGLAKIYAMH 63
 DB 54 LASLKEASESLKRLIEERAKLHDEVLQVAREYALAGQEFMKTRRLKGNKVLICMDV 113
 QY 64 ATDSKLVSASODKRLIYWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGIDNNCS 123
 DB 114 CKDKRRIYSSQDQRLIYWDFTTNKEHAYMPTTWMACAYAPSGNFVACGGIDNNCSV 173
 QY 124 YNL--KSRBEGNVKVSSELSAHTGYLSCCRFLD-DNNITVSSGDTTCALMDITGQOKTYP 180
 DB 174 YPLTFDKNNENAAKKKSYAMHTNYLSACSFNDSMDQLITFASDGTTCALMDVSGQLQSFH 233
 QY 181 VGHGCD--CNSLAVSPDENLFTSGACDASAKLMDVREGRCROFTGHEDINACIFPPNG 238
 DB 234 HGGADVLCLELAPSEGTFTFVSGSDRMATFWDKMSGVHVOVSFEHDSVSKRHPGCD 293
 QY 239 EAICTGSDASCRFLDLRADDELICFSHESIIGITVSFSLSGRLIFAGYDFKNCVWDS 298
 DB 294 DAFASGSDDACRLYDLRADREVAIVFAKESITIFGVNSVDFSVSGRLIFAGYDYNLMDT 353
 QY 299 MKSERVGLISGHDNRVSLGVTADGMAVATGSDSFLKIWM 339
 DB 354 VLKGSRVSLIFGHENRVSTLRVSPDGTAFCSGSDWDTLRVW 394

RESULT 11
 Q9NEZ1 ID Q9NEZ1 PRELIMINARY; PRT; 346 AA.
 AC Q9NEZ1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.
 OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Calliphoridae; Calliphora.
 RN NCBI_TaxID=7373;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=EYE;
 RA Schulz S., Huber A., Schwab K., Paulsen R.;
 RT "A novel Ggamma subunit isolated from *Drosophila* constitutes a visual G
 protein gamma subunit of the fly compound eye."
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A0250442; CAB76452.1; -.
 DR InterPro: IPR000364; -.

Db 127 LDSVCSIFNLSPTDRDGNLWMSRLSGHKGYSSCQVPEEDTHLITGSGDQCYLMI 186
 QY 172 ETGQKTVF-----VGHGTGCKSLAVS-PDRNLITSGACDASAKIMVREGT-CRQTFPG 224
 Db 187 TTGLRTSVGGEFOSGHADVLSTISNSNSKRLVSGSCDATALMDTRASAVAFTHG 246
 QY 225 HESDIAVAFEPFNGALCTGSDASCRFLFDRAODELICS---HSTIGTITVAFTS 281
 Db 247 HEDVAVSVKFFPDGNGRFGTSGDCTCRFLDRIHQHQLQYNOOHENAHVTSIAFTS 306
 QY 282 GLLTLAGTGNDCYVMDTLAKVYLVNLGSLONSHERTICLMSADGALCTGSMIDNLK 337
 Db 307 GLLTLAGTGNDCYVMDTLAKVYLVNLGSLONSHERTICLMSADGALCTGSMIDNLK 337
 QY 338 TW 339
 Db 367 TW 368

RESULT 14
 Q9VM29 PRELIMINARY: PRT: 346 AA.
 AC 09VM29;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAR-2001 (TREMblrel. 13, Last sequence update)
 DE GBETA76C PROTEIN
 GN G-BETA-76C OR GBETA76C OR CG8770.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Ephyroptera; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC NCLTaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananthites P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Sutton G.G., Wortman J.R., Richards S., Ashburner R., Henderson S.N.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Adair J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burdick J.M., Busam D.A., Butler H., Cadieu E., Cantrell D., Chandra I.,
 RA de Pablo B., Delcher A., Deng Z., Davenport L.B., Davies A., Datta I.,
 RA Dodson K.J., Evangelista C.C., Ferraz C., Ferrel J., Garg N.S., Gelpi W.M., Glasner K.,
 RA Glodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ideguchi C.,
 RA Jaiswal M., Kalish J., Karpen G.H., Ke Z., Kennison J.A., Klotz S.M.,
 RA Kimmel B.E., Kodera K., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liou X., Maitte B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mount S.M., Moy M., Murphy B., Murphy C., Morris J., Moshrefi A.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "the genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003516; AAF49124.1; -
 DR HSSP; P04901; 1TBG
 DR Flybase; FBgn0004623; G-beta-76C.
 DR InterPro; IPR001632; -
 DR InterPro; IPR001680; -
 DR Pfam; PF004400; WD40; 7.
 DR PRINTS; PR00319; GPOTENB.
 DR PROSITE; PS00320; GPOTENBPT.
 DR SMART; SM00320; WD40; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 346 AA; 38335 MW; E9B2D937EC3A707 CRC64;

Query Match 45.0%; Score 814; DB 5; Length 346;
 Best Local Similarity 42.8%; Pred. No. 5,46-68;
 Matches 145; Conservative 81; Mismatches 111; Indels 2; Gaps 1;
 QY 3 EMDLQNEAEOLKQIADARACADVTLAELVSGLEVGRVOMRTRLRGLAKIYAMH 62
 Db 7 EFOKLDEINMGIMKRFDDQKSRADCTLDKCGDMGVDFKIFSSKILKGIHKNVSVH 66
 QY 63 WATDSKILVSAOQGLIWDSTYTNKVAHAPRSMWYTCAYAPSGNFVACGGIDNMCS 122
 Db 67 FAGDSRHCYVSGSLDGKLIWDVTANKVQIIPRSMWYTCAYAPSGNFVACGGIDNMCS 126
 QY 123 IYNKSRK-GNPKVRELSAHNGYLSGCRFLDNNITVSGDTTCALMIEFGQKTVF 180
 Db 127 YVDVNNRDSAGVAKVYKELMGTEGFLSSCRFLDGGHILITGSGDMKICHMDEGKATMDF 186
 QY 181 VGHGTGCKSLAVSPDNFLISGACDASAKIMVREGTCTGTFGSHSDINACFPNGEA 240
 Db 187 NGHAGDIALISLSPDKKTYITGVSVDKAKIMVREGTCTGTFGSHSDINACFPNGEA 240
 QY 241 ICGSDASCRFLDRAODELICSHEHSIIIGITVAFTSGLTFAGYDPCNVWMSM 300
 Db 247 FASGCEDDTARWYDLRAQOIAQEPQKMTGTSALSTSGRYLMCGIGBNVHSDTM 306
 QY 301 KSERVGIISGHDNVSICLGYTAGMAVANGSWDSFLKIV 339
 Db 307 KORHGTGLSHENKTTICISLCPMGCIASLWSDQVRLM 345

RESULT 15
 Q9FV61 PRELIMINARY: PRT: 377 AA.
 AC 09FV61;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DE HETTEROTRIMERIC GTP-BINDING PROTEIN SUBUNIT BETA 1.
 OS Nicotiana tabacum (common tobacco).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliopsida; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Solanales; Solanales; Nicotiana.
 RN NCB1_TaxID=4097;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SAMSUN; TISSUE=HAIRY ROOT;
 RX MEDLINE=21002315; PubMed=11126570;
 RA Ando S., Takumi S., Ueda Y., Ueda T., Mori N., Nakamura C.,
 RT "Nicotiana tabacum cDNAs encoding alpha and beta subunits of a
 RL heterotrimeric GTP-binding protein isolated from hairy root tissues."
 DR EMBL; AF249743; AAG12330.1; -
 SQ SEQUENCE 377 AA; 40914 MW; 7052089F40A1707E CRC64;

Query Match 44.7%; Score 809; DB 10; Length 377;
 Best Local Similarity 45.1%; Pred. No. 1,8e-67;
 Matches 161; Conservative 72; Mismatches 98; Indels 26; Gaps 9;

us-09-492-029-5.rsp

Search completed: September 28, 2001, 10:34:07
Job time: 282 sec